

**STIC-Biot ch/Ch mLib**

92268

**From:** Li, Ruixiang  
**Sent:** Wednesday, April 23, 2003 6:16 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search of Application NO: 09/898,586

Please do a standard search on SEQ ID NO: 23 against commercial nucleic acid databases.

Thank you very much!

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**Technical Info. Specialist**  
CM1 6A04  
703-308-3524

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 4/24  
Date Completed: 5/2  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

**TYPE OF SEARCH:**  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

**VENDOR/COST (where applic.)**  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





XX 13-JAN-2000; 2000US-0175989.  
 PR 14-JAN-2000; 2000US-0176134.  
 PR 25-JAN-2000; 2000US-0177839.  
 PR 26-JAN-2000; 2000US-0178191.  
 PR 14-JUL-2000; 2000US-0218324.  
 PR 24-JUL-2000; 2000US-0220253.  
 PR 25-JUL-2000; 2000US-0220590.  
 XX (CURA-) CURAGEN CORP.  
 XX PT Padigaru M, Prayaga SK, Taupier RJ, Mishra V, Tchernev VT;  
 PT Spytek KA, LJ L;  
 XX DR WPI; 2001-451859/48.  
 DR P-PSDB; AAU05142.  
 XX PT New NOVX polypeptides and poly nucleotides, useful for treating or  
 PT preventing disorders of the neuro-olfactory system, cancer and multiple  
 PT sclerosis -  
 XX PS Claim 9; Page 55; 141pp; English.  
 XX The sequence represents the coding sequence of human odorant receptor  
 CC (OR)-like protein, NOV12. The NOV12 Polypeptide, nucleic acid and  
 CC antibody are useful as therapeutics, particularly in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease, which  
 CC includes a pathology associated with NOV12 polypeptide. The NOV12 nucleic  
 CC acid and polypeptide are especially useful in therapeutic or  
 CC prophylactic applications for disorders of the neuro-olfactory system,  
 CC e.g. those induced by trauma, surgery and/or neoplastic disorders. The  
 CC DNA encoding the protein is useful in gene therapy for treating the  
 CC above conditions. Furthermore, the nucleic acids and polypeptides are  
 CC useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus  
 CC cancer, immune response, acquired immunodeficiency syndrome (AIDS),  
 CC asthma, Crohn's disease, multiple sclerosis or Albright hereditary  
 CC osteodystrophy. These are also useful in developing powerful assay  
 CC system for functional analysis of various human disorders, as well as  
 CC in diagnostic applications.  
 XX SQ Sequence 1014 BP; 219 A; 281 C; 216 G; 298 T; 0 other;

Query Match 97.7%; Score 991; DB 22; Length 1014;  
 Best Local Similarity 99.8%; Pred. No. 4.3e-287; Mismatches 1013; Conservative 0; Indels 2; Gaps 2;

QY 1 TAAACACTTCTAAACCATGAGCATTAACTGTATTCTCTGTICATAGGGATATGGGG 60  
 Db 1 TAAACACTTCTCTAAACCATGAGCATTAACTGTATTCTCTGTICATAGGGATATGGGG 60  
 QY 61 GACAATATAACATCCATCACAGAGTTCCTCTACTGGGATTCCCGTTGGCCCAAAGATT 120  
 Db 61 GACAATATAACATCCATCACAGAGTTCCTCTACTGGGATTCCCGTTGGCCCAAAGATT 120  
 QY 121 CAGATGCTCCCTTGGCTCTTCCCTGTTCTACGGTCTCACCTGCTGGGGAAACGGG 180  
 Db 121 CAGATGCTCCCTTGGCTCTTCCCTGTTCTACGGTCTCACCTGCTGGGGAAACGGG 180  
 QY 181 ACCATACTGGGCTCATCTCACTGGACTCCAGCCCCC-TGTACTTCTTCCTC 239  
 Db 181 ACCATACTGGGCTCATCTCACTGGACTCCAGCCCCCAG 240  
 QY 240 TCAACACCTGGCGGTGCTGACATGGCTTACGCCCTGCCGCTGCAACACGGTCCCCGGATGGTG 299  
 Db 241 TCAACACCTGGCGGTGCTGACATGGCTTACGCCCTGCCGCTGCAACACGGTCCCCGGATGGTG 300  
 QY 300 AACCTCTCTGCAAGCCCATCTCTTGGGGCGCATGATGAGACCTTCTG 359  
 Db 301 AACCTCTGCAAGCCCATCTCTTGGGGCGCATGATGAGACCTTCTG 360  
 QY 360 TTTCCACTTTGCTGTCAGAATGTCCTCTCTGGTGTGATGTCCTATGATCTGTAC 419

RESULT 2  
 ID AAS09955  
 ID AAS09955 standard; DNA; 1012 BP.

XX AC AAS09955;  
 XX DT 24-OCT-2001 (first entry)  
 DE DNA encoding human odorant receptor (OR)-like protein, NOV11.  
 KW Odorant receptor; human; OR; NOV11; therapeutic; neuro-olfactory system;  
 KW trauma; surgery; neoplastic disorder; gene therapy; adenocarcinoma;  
 KW lymphoma; prostate cancer; uterus cancer; immune response; asthma; AIDS;  
 KW acquired immunodeficiency syndrome; Crohn's disease; multiple sclerosis;  
 KW Albright hereditary osteodystrophy; diagnostic; ds.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT 5' UTR 1..53  
 FT CDS 54..986  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /\*product= "odorant receptor-like protein, NOV11"  
 FT /\*tag= c  
 FT 3' UTR 98..1012  
 FT /\*tag= c  
 PN WO200151632-A2.  
 PD 19-JUL-2001.

Db 361 TTTCCACTTTGCTGTCAGAATGTCCTCTCTGGTGTGATGTCCTATGATCTGTAC 420  
 QY 420 GTGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGCATCACC 479  
 Db 421 CTGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGCATCACC 480  
 QY 480 CTCGGGGTACTCTGGACACTGGAGTCCTTTATCCTGTATCATCTGTGTACTT 539  
 Db 481 CTGGGGTACTCTGGACACTGGAGTCCTTTATCCTGTATCATCTGTGTACTT 540  
 QY 540 CTACCTTACCTCTGTAGGCCCCAGAAATTATCACTTTTTGTGAATCTGGC 599  
 Db 541 CTACCTTACCTCTGTAGGCCCCAGAAATTATCAC-TTTTTGTGAATCTGGC 599  
 QY 600 TGTCTCAAACCTGGCTGTGAGATACCCACATCAATGAGAACATGGCTTGCGGGAGC 659  
 Db 600 TGTCTCAAACCTGGCTGTGAGATACCCACATCAATGAGAACATGGCTTGCGGGAGC 659  
 QY 660 AATTCTGGCTGGGGACCCCTGTCCACAAATGTTAGTT 719  
 Db 660 AATTCTGGCTGGGGACCCCTGTCCACAAATGTTAGTT 719  
 QY 720 TGCTATCCTCAGATCCAATCAAGGGAGTTGAGGAAAGCCTCTGCACCTGCTCTC 779  
 Db 720 TGCTATCCTCAGATCCAATCAAGGGAGTTGAGGAAAGCCTCTGCACCTGCTCTC 779  
 QY 780 CCACCTCTGTGTGATGGACTCTTTATGGCACACGCCATTATCATGTATGTGGACCCAG 839  
 Db 780 CCACCTCTGTGTGATGGACTCTTTATGGCACACGCCATTATCATGTATGTGGACCCAG 839  
 QY 840 ATATGGAAACCCAAAGGAGGAGAAGAATATCTCTGCTGTTACAGCCTCTTAATCC 899  
 Db 840 ATATGGAAACCCAAAGGAGGAGAAGAATATCTCTGCTGTTACAGCCTCTTAATCC 899  
 QY 900 CATGCTCAATCCCTTATCTGTAGCTTAGGAACTCAGAAGTGGAGAATACTTTGAAGAG 959  
 Db 900 CATGCTCAATCCCTTATCTGTAGCTTAGGAACTCAGAAGTGGAGAATACTTTGAAGAG 959  
 QY 960 AGTGGCTGGAGTAGAAGGGTTATGAAAGGATTATGGCATGTGACTGACAA 1014  
 Db 960 AGTGGCTGGAGTAGAAGGGCTTATGAAAGGATTATGGCATGTGACTGACAA 1014

QY	361	TTTCACTTTGCTGTCAGAAATGTCCTCTGGGGTATGTCCTATGACTGTACG	420
PR	13-JAN-2000;	20000S-0175989-	
PR	14-JAN-2000;	20000S-0176134-	
PR	25-JAN-2000;	20000S-0177839-	
PR	26-JAN-2000;	20000S-0178191-	
PR	26-JAN-2000;	20000S-0178227-	
PR	14 JUL-2000;	20000S-0218324-	
PR	24 JUL-2000;	20000S-0220253-	
PR	25-JUL-2000;	20000S-0220590-	
XX		(CURA-) CURAGEN CORP.	
PA			
PI		Padigaru M, Prayaga SK, Taupier RJ, Mishra V, Tchernev VT;	
PI		Spytek KA, Li L;	
WPI		WPI; 2001-451859/48.	
DR		p-PSDB; AAU05141.	
XX			
PT		New NOVX polypeptides and polynucleotides, useful for treating or preventing disorders of the neuro-olfactory system, cancer and multiple sclerosis -	
PT		claim 9; Page 52; 141PP; English.	
XX			
CC		The sequence represents the coding sequence of human odorant receptor (OR)-like protein, NOV11. The NOV11 polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOV11 polypeptide. The NOV11 nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders of the neuro-olfactory system, e.g., those induced by trauma, surgery and/or neoplastic disorders. The DNA encoding the Protein is useful in gene therapy for treating the above conditions. Furthermore, the nucleic acids and polypeptides are useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications.	
XX			
SQ		Sequence 1012 BP; 219 A; 281 C; 215 G; 297 T; 0 other;	
Query Match		97.4%; Score 987.4; DB 22; Length 1012;	
Best Local Similarity		99.7%; Pred. No. 5.2e-286;	
Matches		1010; Conservative 0; Mismatches 1; Indels 2; Gaps 2;	
QY	2	AAACACTTCTCTAAACCATGAGCTAACTGATTCTCTGTCAAGGGATATGGGG 61	
Db	1	AAACACTTCTCTAAACCATGAGCTAACTGATTCTCTGTCAAGGGATATGGGG 60	
QY	62	ACAAATACATCCATCACAGAGTCCCTACTGGATTCCCGTGGCCAAAGGATC 121	
Db	61	ACAAATACATCCATCACAGAGTCCCTACTGGATTCCCGTGGCCAAAGGATC 120	
QY	122	AGATGCTCCCTTGGGCTCTCCACTGGGATTCCCCGTGGCCAAAGGATC 181	
Db	121	AGATGCTCCCTTGGGCTCTCCACTGGGATTCCCCGTGGCCAAAGGATC 180	
QY	182	CCATACTGGGGCTCATCTCACTGGACTCCAGCTGACGCCCT-GTACTTCCCT 240	
Db	181	CCATACTGGGGCTCATCTCACTGGACTCCAGCTGACGCCCT-GTACTTCCCT 240	
QY	241	CACACCTGGGGTCTCGACATCGCCTACGCCCTGCAACACGGTCCCCGATGCTGGTA 300	
Db	241	CACACCTGGGGTCTCGACATCGCCTACGCCCTGCAACACGGTCCCCGATGCTGGTA 300	
QY	301	ACCTCCTGATCCAGCCAAAGCCATCTCTTGGGGCGATGCGAGACCTTCTGT 360	
Db	301	ACCTCCTGATCCAGCCAAAGCCATCTCTTGGGGCGATGCGAGACCTTCTGT 360	

XX XX  
 PD 19-JUL-2001.  
 XX PR 16-JAN-2001; 2001WO-US01513.  
 XX PR 13-JAN-2000; 2000US-0175989.  
 PR 14-JAN-2000; 2000US-0176134.  
 PR 25-JAN-2000; 2000US-0177839.  
 PR 26-JAN-2000; 2000US-0178191.  
 PR 26-JAN-2000; 2000US-0178227.  
 PR 14-JUL-2000; 2000US-0220253.  
 PR 24-JUL-2000; 2000US-0220590.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Padigaru M, Prayaga SK, Taupier RJ, Mishra V, Tchernev VT;  
 PI Spytek KA, Li L;  
 DR WPI; 2001-451859/48.  
 DR P-PSDB; AAU05132.  
 XX PT New NOVX polypeptides and polynucleotides, useful for treating or  
 PT preventing disorders of the neuro-olfactory system, cancer and multiple  
 XX scleriosis -  
 XX PS Claim 9; Page 15; 141pp; English.  
 XX The sequence represents the coding sequence of human odorant receptor  
 CC (OR)-like protein, NOV2. The NOV2 polypeptide, nucleic acid and antibody  
 CC are useful as therapeutics, particularly in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease, which  
 CC includes a pathology associated with NOV2 polypeptide. The NOVX nucleic  
 CC acid and polypeptides are especially useful in therapeutic or  
 CC prophylactic applications for disorders of the neuro-olfactory system,  
 CC e.g. those induced by trauma, surgery and/or neoplastic disorders. The  
 CC DNA encoding the protein is useful in gene therapy for treating the  
 CC above conditions. Furthermore, the nucleic acids and polypeptides are  
 CC useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus  
 CC cancer, immune response, acquired immunodeficiency syndrome (AIDS),  
 CC asthma, Crohn's disease, multiple sclerosis or Albricht hereditary  
 CC osteodystrophy. These are also useful in developing powerful assay  
 CC system for functional analysis of various human disorders, as well as  
 CC in diagnostic applications.  
 XX Sequence 1040 BP; 229 A; 285 C; 221 G; 305 T; 0 other;  
 XX Query Match 97.0%; Score 983.6; DB 22; Length 1040;  
 XX Best Local Similarity 99.4%; Pred. No. 7.3e-285;  
 XX Matches 1008; Conservative 0; Mismatches 4; Indels 2; Gaps 2;  
 QY 1 TAAACACTCTCTAAACCATGAGCATAACTGGATTCTCTGTGTCATAGGGATATGGGG 60  
 DB 28 TAAACACTCTCTAAACCATGAGCATAACTGGATTCTCTGTGTCATAGGGATATGGGG 87  
 QY 61 GACAATATAACATCCATCACAGAGTCTCTACTGGGATTCCGGTGGCCCAAGGATT 120  
 DB 88 GACAATATAACATCCATCACAGAGGATTCCGGTGGCCCAAGGATT 147  
 QY 121 CAGATGCTCTCTTGGGCTCTCCCTGCTTACGTTACCCCTGCTGGGAACGGG 180  
 DB 148 CAGATGCTCTCTTGGGCTCTCCCTGCTTACGTTACCCCTGCTGGGAACGGG 207  
 QY 181 ACCATACTGGGCTCATCTCACTGGACTCAGACTGCACGCCCTACGGTCTC 239  
 DB 208 ACCATACTGGGCTCATCTCACTGGACTCAGACTGCACGCCCTACGGTCTC 267  
 QY 240 TCACACCTGGGCTCTGGACATGGCTACCCCTGCAACACGGTCCCCGGATGCTGGT 299  
 DB 268 TCACACCTGGGCTCTGGACATGGCTACCCCTGCAACACGGTCCCCGGATGCTGGT 327  
 QY 300 AACCTCTGCAAGCCAAGCCCATCTCCTTGGGGCCATGATGCAGACCTTCTG 387  
 XX  
 Db 328 AACCTCTGCAAGCCAAGCCCATCTCCTTGGGGCCATGATGCAGACCTTCTG 387  
 QY 360 TTTCCACTTTGTCGICACAGAAATGTCCTCTCTGGTGTATGATCTGTC 419  
 Db 388 TTTCCACTTTGTCGICACAGAAATGTCCTCTCTGGTGTATGATCTGTC 447  
 QY 420 GTGGCCATCTGCCACCCCTCGATATTGGCCATCATGACCTGGAGAGTCTGCATCACC 479  
 Db 448 GTGGCCATCTGCCACCCCTCGATATTGGCCATCATGACCTGGAGAGTCTGCATCACC 507  
 QY 480 CTCGCGGTGACTCTCTGGACACTGGAGCTGGTACTT 539  
 Db 508 CTCGCGGTGACTCTCTGGACACTGGAGCTGGTACTT 567  
 QY 540 CTACCTTACCTCTGTAGGCCAGAAATTACACTTTTGTGAATCTGGC 599  
 Db 568 CTACCTTACCTCTGTAGGCCAGAAATTACACTTTGTGAATCTGGC 626  
 QY 600 TGTCTCTCAAACCTGGCTGTGAGATACCCACATCAATGAGAACATGGCTTGGCGGGAGC 659  
 Db 627 TGTCTCTCAAACCTGGCTGTGAGATACCCACATCAATGAGAACATGGCTTGGCGGGAGC 686  
 QY 660 AATTCTGGCTGGGACCTGTGCCAACATTGAGTTCAATATGTC 719  
 Db 687 AATTCTGGCTGGGACCTGTGCCAACATTGAGTTCAATATGTC 746  
 QY 720 TGCTATCTTCAGATCCAATCAAGGGAGTTCAAGGAAGTTCAGAGGAAGCTTCAGGGAAAGCCCTCCGACCTGCTTC 779  
 Db 747 TGCTATCTTCAGATCCAATCAAGGGAGTTCAAGGAAGTTCAGAGGAAGCCCTCCGACCTGCTTC 806  
 QY 780 CCACCTCTGTGATGGACTCTTATGGCACAGCCATTATCATGATGTTGGACCCAG 839  
 Db 807 CCACCTCTGTGATGGACTCTGTTATGGCACAGCCATTATCATGATGTTGGACCCAG 866  
 QY 840 ATATGGGAAACCCAAAGGAGCAGAAAGAATCTCCIGCTTACAGCCTCTTAATCC 899  
 Db 867 ATATGGGAAACCCAAAGGAGCAGAAAGAATCTCCIGCTTACAGCCTCTTAATCC 926  
 QY 900 CATGCTCAATCCCCATTATGTGAGTTAGGAACTCAGAAGTGAAGAATACTTGAAGAG 959  
 Db 927 CATGCTCAATCCCCATTATGTGAGTTAGGAACTCAGAAGTGAAGAATACTTGAAGAG 986  
 QY 950 AGTGTCTGGGAGTAGAAAGGGCTTATGAAAGGATATGGCATGTGACTGACA 1013  
 Db 987 AGTGCTGGGAGTAGAAAGGGCTTATGAAAGGATATGGCATGTGACTGACA 1040  
 XX  
 RESULT 4  
 ABA09073/C  
 ID ABA09073 standard; cDNA; 1315 BP.  
 XX  
 AC ABA09073;  
 XX DT 11-JAN-2002 (first entry)  
 XX DE Human olfactory receptor homologue-encoding cDNA, SEQ ID NO:849.  
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenes; proliferation; metastasis; cancer; tumour; haemopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; viricide; antibacterial; antifungal; pulmonary; antiulcer; ss.  
 XX OS Homo sapiens.

PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US03800.  
 XX PR 03-FEB-2000; 2000US-0495914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Tang YT, Liu C, Drmanac RT;  
 XX DR WPI; 2001-457740/49.  
 DR P-PSDB; ABB11829.  
 XX PT Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -  
 PT  
 XX PS Claim 1; Page 753; 1963pp; English.  
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; actin- or inhibitor-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include disorders, haemopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

XX Sequence 1315 BP; 380 A; 281 C; 360 G; 294 T; 0 other;

SQ

Query Match 92.9%; Score 942; DB 22; Length 1315;  
 Best local similarity 99.6%; Pred. No. 2.6e-272; Matches 986; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

QY 1 TAACACTTCTCTAAACCATGAGCATTAACGTGATTCTCTGTGATAGGGATATGGGG 60  
 989 TAACACTTCTCTAAACCATGAGCATTAACGTGATTCTCTGTGATAGGGATATGGGG 930

QY 61 GACAATATAACATCCATCACAGAGTTCTACTGGGATTCCCGTGGCCAAAGGATT 120  
 929 GACAATATAACATCCATCACAGAGTTCTACTGGGATTCCCGTGGCCAAAGGATT 870

QY 121 CAGATGCTCTTGGCTCTCTCCGTCTACGTCTCACCCGTGGGAACGGG 180  
 Db 869 CAGATGCTCTTGGCTCTCTCCGTCTACGTCTCACCCGTGGGAACGGG 810

QY 181 ACCATACTGGGCTCATCTACTGGACTCCAGACTGACGGCCC-TGTACTTCTTC 239  
 Db 809 ACCATACTGGGCTCATCTACTGGACTCCAGACTGACGGCCCATGTACTTCTTC 750

QY 240 TCACACCT-GGGGTGTCGACATGCCAACACGGTCCCCGATGCTGT 298  
 Db 749 TCACACCTGGGGGTGTCGACATGCCAACACGGTGGGGGGATGCTGT 690

QY 299 GAACCTCCTGCATCCAGCAAGCCATCTCCTTGCGGCCATGATGCCAGACCTTCT 358  
 Db 689 GAACCTCCTGCATCCAGCAAGCCATCTCCTTGCGGCCATGATGCCAGACCTTCT 630

QY 478 CCCTCGGGTGACTTCTGGACCACTGGAGTCTCTCCCTGGTGTGATGCTCTATGTA 418  
 Db 509 CCCTCGGGTGACTTCTGGACCACTGGAGTCTCTTGATTCTGATGTCGATCA 510

QY 538 TTCTACCTTACCCCTCTGTGAGGCCCCAGAAATTACTACTTTTTGTAATCTTG 597  
 Db 449 TTCTACCTTACCCCTCTGTGAGGCCCCAGAAATTATCAC-TTTTTTGAAATCTTG 391

QY 598 GCTGTCTCAACCTGCCTGTGAGATACCCACATCAATGAGAACATGGCTTGGCGGA 657  
 Db 390 GCTGTCTCAACCTGCCTGTGAGATACCCACATCAATGAGAACATGGCTTGGCGGA 331

QY 658 GCAATTCTGGGCTGGGGACCCCTGTCCACAAATGTAGTTCATATATGTGCATCTC 717  
 Db 330 GCAATTCTGGGCTGGGGACCCCTGTCCACAAATGTAGTTCATATATGTGCATCTC 271

QY 718 TGTGCTATCCTCTGAGTCCAACTCAAGGGAAGTTCAGGAAGGCCTCTGCACCTGCTC 777  
 Db 270 TGTGCTATCCTCTGAGTCCAACTCAAGGGAAGTTCAGGAAGGCCTCTGCACCTGCTC 211

QY 778 TCCCACTCTGTGATGGACTCTTTATGGCACACGCCATTATCATGTATGTGACCC 837  
 Db 210 TCCCACTCTGTGATGGACTCTTTATGGCACACGCCATTATCATGTATGTGACCC 151

QY 838 AGATATGGGACCCAAAGGAGCAGAGAAATATCTCTGTGTTCACAGGCTCTTAAT 897  
 Db 150 AGATATGGGACCCAAAGGAGCAGAGAAATATCTCTGTGTTCACAGGCTCTTAAT 91

QY 898 CCCATGCTCAATCCCTTATCTGTAGTCTAGGAACTCAGAGTGAGAAATACTTGAAG 957  
 Db 90 CCCATGCTCAATCCCTTATCTGTAGTCTAGGAACTCAGAGTGAGAAATACTTGAAG 31

QY 958 AGAGTGCTGGGAGTAGAAGGGCTTATGA 987  
 Db 30 AGAGTGCTGGGAGTAGAAGGGCTTATGA 1

RESULT 5  
 AAFF58613  
 ID AAFF58613 standard; CDNA; 974 BP.  
 XX AC AAFF58613;  
 XX DT 24-APR-2001 (first entry)  
 XX DE Human RECAP polynucleotide, SEQ ID NO: 41.  
 XX KW Human; RECAP; receptors and associated proteins; cerebroprotective;

KW nootropic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;  
 KW antidiabetic; immunostimulant; immunomodulator; antiinflammatory;  
 KW antithyroid; immunosuppressive; nephrotropic; antigout; thyromimetic;  
 KW cytostatic; antibacterial; viricide; fungicide; protozoacide; antiarteriosclerotic; hepatotropic; gene therapy; infection; cancer; ss.  
 XX OS Homo sapiens.  
 XX PN WO200107612-A2.  
 XX PD 01-FEB-2001.  
 XX PF 21-JUL-2000; 2000WO-US20035.  
 XX PR 21-JUL-1999; 99US-0145232.  
 PR 07-OCT-1999; 99US-0158578.  
 PR 12-NOV-1999; 99US-0165192.  
 XX PA ( INCY - ) INCYTE GENOMICS INC.  
 XX AU-YOUNG J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;  
 PI Baughn MR, Lu DAM, Hillman JL, Patterson C, Lal P;  
 XX DR P-PSDB; AAB68889.  
 XX PS Claim 5; Page 125-126; 128pp; English.  
 XX PT Novel receptors and associated proteins for diagnosis and treatment of  
 PT neurological disorders, immunological disorders including autoimmune/  
 PT inflammatory disorders and cell proliferative disorders such as cancer  
 PT -  
 XX PT DR  
 XX PS  
 CC The present sequence encodes a human RECAP (receptors and associated  
 CC proteins) polypeptide. RECAP polynucleotides and polypeptides are useful  
 CC in the diagnosis, treatment and prevention of neurological disorders  
 CC such as stroke, Alzheimer's disease, Pick's disease, Huntington's  
 CC disease, dementia, Parkinson's disease, Down's syndrome, amyotrophic  
 CC lateral sclerosis, multiple sclerosis, bacterial and viral meningitis,  
 CC CJD (Creutzfeldt Jakob disease), GSS (Gerstmann -Straussler-Scheinker  
 CC syndrome); immunological disorders, including autoimmune/inflammatory  
 CC disorders such as AIDS, DiGeorge's syndrome, severe combined  
 CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's  
 CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,  
 CC diabetes mellitus, Good pasture's syndrome, gout, Grave's diseases,  
 CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral,  
 CC bacterial, fungal, parasitic, protozoal, and helminth infections; and  
 CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,  
 CC cirrhosis, hepatitis and cancer.  
 XX SQ Sequence 974 BP; 206 A; 270 C; 214 G; 284 T; 0 other;  
 Query Match 92.3%; Score 935; DB 22; Length 974;  
 Best Local Similarity 99.8%; Pred. No: 1.4e-270;  
 Matches 958; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
 QY 55 ATGGGGACACATAACATCCATCACAGAGTTCTCTACTGGGATTCCCGTTGGCCA 114  
 DB 1 ATGGGGACACATAACATCCATCACAGAGTTCTCTACTGGGATTCCCGTTGGCCA 60  
 QY 115 AGGATTCAGATGCTCTTGGGCTCTCTCCCTGTTCTACGCTTCAACCTGCTGGG 174  
 DB 61 AGGATTCAGATGCTCTTGGGCTCTCTCCCTGTTCTACGCTTCAACCTGCTGGG 120  
 QY 175 AACGGGACATACTGGGCTCATCTACTGGGACTCCAGACTGCACGCCCA-TGTTACTC 233  
 DB 121 AACGGGACATACTGGGCTCATCTACTGGGACTCCAGACTGCACGCCCA-TGTTACTC 180  
 QY 234 TTCTCTCACACCTGGGCTGTCGACATCGCCTACGCCATCGCTG 293  
 DB 181 TTCTCTCACACCTGGGCTGTCGACATCGCCTACGCCATCGCTG 240  
 QY 294 CTGGTGAACCTCTGCATCCAGCCACAGCCATCTCTGGGGCCATGATGCCAGACC 353

DB 241 CTGGTGAACCTCTGCATCCAGCCATCTCTGGGGCCATGATGCCAGACC 300  
 QY 354 TTCTCTTTCACATTGGTCACTGTCACAGATGTCCTCCCTGGGGTATGTCCTATGAT 413  
 DB 301 TTCTCTTTCACATTGGTCACTGTCACAGATGTCCTCCCTGGGGTATGTCCTATGAT 360  
 QY 414 CTGTAOGGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGC 473  
 DB 361 CTGTAOGGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGC 420  
 QY 474 ATCACCTCGGGGACTTCGACCTGGGACTCTGGGACACTGGAGCTCTTTATCCTTGATTCATCTTG 533  
 DB 421 ATCACCTCGGGGACTTCGACCTGGGACACTGGAGCTCTTTATCCTTGATTCATCTTG 480  
 QY 534 TTACTTCTACCTTACCCCTCTGTAGGCCCCAGAAATTACTTACTTTTGAAAT 593  
 DB 481 TTACTTCTACCTTACCCCTCTGTAGGCCCCAGAAATTATCCT-TTTTTTGTGAAAT 539  
 QY 594 CTGGGCTGTTCCAAACTGGCTGTGCGAGATACCCACATCAATGAGAACATGGCTTG 653  
 DB 540 CTGGGCTGTTCCAAACTGGCTGTGCGAGATACCCACATCAATGAGAACATGGCTTG 599  
 QY 654 CGGAGCAATTCTGGCTGGGACCCCTGTCCACAAATTGTTCAATATGTCAT 713  
 DB 600 CGGAGCAATTCTGGCTGGGACCCCTGTCCACAAATTGTTCAATATGTCAT 659  
 QY 714 CCTCTCTGCTATCCTTCAGATCCAATCAAGGAAGTTCAGAGGAAGGCCTCTGCACCTG 773  
 DB 660 CCTCTCTGCTATCCTTCAGATCCAATCAAGGAAGTTCAGAGGAAGCCTCTGCACCTG 719  
 QY 774 CTTCCTCCACCTCTGTGTGATGGACTCTTATGGCACAGCCATTATCAGTATGTCAT 833  
 DB 720 CTTCCTCCACCTCTGTGTGATGGACTCTTATGGCACAGCCATTATCAGTATGTCAT 779  
 QY 834 ACCCAGATATGGAACCCCAAGGGAGAGAAATATCCTGCTGTTACAGCCTT 893  
 DB 780 ACCCAGATATGGAACCCCAAGGGAGAGAAATATCCTGCTGCTGTTACAGCCTT 839  
 QY 894 TAATCCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACCTCAGAAAGTGAAGAATACTTT 953  
 DB 840 TAATCCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACCTCAGAAAGTGAAGAATACTTT 899  
 QY 954 GAAGAGAGTGTGGAGTAGAAGGGCTTATGAAAGGATTATGGCATTTGTGACTGACA 1013  
 DB 900 GAAGAGAGTGTGGAGTAGAAGGGCTTATGAAAGGATTATGGCATTTGTGACTGACA 959  
 RESULT 6  
 AAH32365  
 ID AAH32366 standard; DNA; 930 BP.  
 XX AC AAH32366;  
 XX DT 30-JUL-2001 (first entry)  
 XX DE Human olfactory receptor polynucleotide, SEQ ID NO: 939.  
 XX KW Human; olfactory receptor; OR; primary scent determination;  
 KW secondary scent determination; polypeptide library; odour receptor;  
 KW scent profile; scent fingerprint; scent representation; ds.  
 XX OS Homo sapiens.  
 XX PN WO200127158-A2.  
 XX PR 06-OCT-2000; 2000WO-US27582.  
 XX PD 19-APR-2001.  
 XX PR 08-OCT-1999; 99US-0158615.  
 PR 24-FEB-2000; 2000US-0184809.  
 XX

PA (DIGI-) DIGISCENTS.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
 XX DR WPI; 2001-290713/30.  
 PT New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -  
 XX PS Claim 8; Page 554; 1857pp; English.  
 XX  
 CC The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The CC polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary CC scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of CC secondary scents and the identification of combinations of odour CC receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called CC a scent fingerprint or scent profile), which may be used to re-create CC and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, CC and can be used for determining differences in the olfactory faculties CC of different individuals.  
 XX  
 SQ Sequence 930 BP; 192 A; 266 C; 201 G; 271 T; 0 other;  
 Query Match 89.3%; Score 905.4; DB 22; Length 930;  
 Best Local Similarity 99.7%; Pred. No. 2.1e-261;  
 Matches 928; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
 QY 55 ATGGGGACAAATAACATCCATCACAGAGTTCCTACTGGATTTCCGGTGGCCA 114  
 1 ATGGGGACAAATAACATCCATCACAGAGTTCCTACTGGATTTCCGGTGGCCA 60  
 QY 115 AGGATTCAAGATGCTCCCTTGGGCTCTTCCTCCCTGTTAGCTCTCACCCCTGCTGGGG 174  
 61 AGGATTCAAGATGCTCCCTTGGGCTCTTCCTGTTAGCTCTCACCCCTGCTGGGG 120  
 QY 175 AACGGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGGCCC-TGACTTC 233  
 Db 121 AACGGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGGCCCATGTACTTC 180  
 QY 234 TTCTCTCACACACCTGGGGTCTGACATCGCTGACACAGGTGCCCGGATG 293  
 Db 181 TTCTCTCACACACCTGGGGTCTGACATCGCTGACACAGGTGCCCGGATG 240  
 QY 294 CTGGTGAACTCTGCATCCAGCCAGGCCATCTCTTGGGGCCATGTCAGACC 353  
 Db 241 CTGGTGAACTCTGCATCCAGCCAGGCCATCTCTTGGGGCCATGTCAGACC 300  
 QY 354 TTCTCTCACCTTGGCCATCTGCCACCCCTCCGATATTGGCATCTGACCTGGAGACTGC 413  
 Db 301 TTCTCTCACCTTGGCCATCTGCCACCCCTCCGATATTGGCATCTGACCTGGAGACTGC 360  
 QY 414 CTGTACGGCATCTGCCACCCCTCCGATATTGGCATCTGACCTGGAGACTGC 473  
 Db 361 CTGTACGGCATCTGCCACCCCTCCGATATTGGCATCTGACCTGGAGACTGC 420  
 QY 474 ATCACCCCTGGGGACTCTCTGGACACTGGACTCTTATCCTGATTCTGTC 533  
 Db 421 ATCACCCCTGGGGACTCTCTGGACACTGGACTCTTATCCTGATTCTGTC 480  
 QY 534 TTACTCTCACCTTACCTTACCCCTCTGAGGGCCAGAAATTATCACTTTTTGTAAT 593  
 Db 481 TTACTCTCACCTTACCCCTCTGAGGGCCAGAAATTATCACTTTTTGTAAT 539  
 QY 594 CTGGCTGTTCTCAAACCTGGCTGTCAGATACCCACATCAATGAGAACATGGCTTGGC 653  
 Db 540 CTGGCTGTTCTCAAACCTGGCTGTCAGATACCCACATCAATGAGAACATGGCTTGGC 599

QY 654 CGGAGCAATTCTGGGACCTCTGTCACAAATGTTCATATATGTCAT 713  
 Db 600 CGGAGCAATTCTGGGCTGTTGGACCCCTGTCACAATGTTCATATATGTCAT 659  
 QY 714 CCTCTGTGCTATCCCTCAGATCCAATCAAGGAAGTCAGAGGAAGCCTCTGCACCTG 773  
 Db 660 CCTCTGTGCTATCCCTCAGATCCAATCAAGGAAGTCAGAGGAAGCCTCTGCACCTG 719  
 QY 774 CTTCTCCCACCTCTGTTGATGGACTCTTATGCCACAGCATTATCATGTATGTTGG 833  
 Db 720 CTTCTCCCACCTCTGTTGATGGACTCTTATGCCACAGCATTATCATGTATGTTGG 779  
 QY 834 ACCAGATATGGAAACCCAAAGGAGCAGAANTATCTCCTGTTACAGCCTCT 893  
 Db 780 ACCCAGATATGGAAACCCAAAGGAGCAGAANTATCTCCTGTTACAGCCTCT 839  
 QY 894 TAATCCCAGTCTCAATCCCTATCTGTTAGTCTTAGGAACTCAGAAGTGGAGATACTTT 953  
 Db 840 TAATCCCATGCTCAATCCCTATCTGTTAGTCTTAGGAACTCAGAAGTGGAGATACTTT 899  
 QY 954 GAAGAGAGTGTGGAGTAGAAAGGGCTTA 984  
 Db 900 GAAGAGAGTGTGGAGTAGAAAGGGCTTA 930

Db ABK65141  
 ID ABK65141 standard; cDNA; 933 BP.  
 XX AC ABK65141;  
 XX DT 02-JUL-2002 (first entry)  
 XX DE cDNA encoding human PHOR1-F5D6.  
 XX KW Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200214501-A2.  
 XX PD 21-FEB-2002.  
 XX PF 17-AUG-2001; 2001WO-US25862.  
 XX PR 17-AUG-2000; 2000US-226241P.  
 XX PA (AGEN-) AGENSYN INC.  
 XX PI Hubert RS, Raitano AB, Faris M, Challita-Eid PM, Ge W;  
 XX DR WPI; 2002-269193/31.  
 XX P-PSDB; AU91543.  
 PT Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene products in tissue sample from subject and comparing it to normal tissue sample -  
 PT sample -  
 XX PS Claim 43; Fig 2b; 250pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human genes designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The CC gene encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding CC PHOR1-F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6 CC polynucleotide and polypeptide sequences are useful in diagnostic and CC therapeutic methods, and compositions for various cancers such as CC prostate cancer. The sequences are useful for inhibiting the growth of CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof CC can be used to elicit an immune response. The present sequence encodes CC human PHOR1-F5D6.

XX	AAH31617
SQ	Sequence 933 BP; 194 A; 265 C; 203 G; 271 T; 0 other;
Query Match	8.9.18; Score 903.6; DB 24; Length 933;
Best Local Similarity	99.4%; Pred. No. 7.4e-261;
Matches	928; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY	55 ATGGGGACAAATAACATCCATCACAGAGTTCTCTACTGGGATTCCCGRTGGCCA 114
Db	1 ATGGGAGACAATAACATCCATCACAGAGAGTTCTCTACTGGGATTCCCGRTGGCCA 60
OY	115 AGGATCAGATGCTCTCTTGGCTCTCCCGTCTACGCTTACCCGTGGG 174
Db	61 AGGATCAGATGCTCTCTTGGCTCTCCCGTCTACGCTTACCCGTGGG 120
QY	175 AACGGGACATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCC-TGTACTTC 233
Db	121 AACGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCCATGTACTTC 180
OY	234 TTCTCTCACACCTGGGGCTGTCGACATCGCCTACGCTTGCAACACGGTGGGGATG 293
Db	181 TTCTCTCACACCTGGGGCTGTCGACATCGCCTACGCTTGCAACACGGTGGGGATG 240
OY	294 CTGGTGAACCTCTGCATCCAGCAAGCCATCTCGTGGGGCATGATCGAGCC 353
Db	241 CTGGTGAACCTCTGCATCCAGCAAGCCATCTCGTGGGGCATGATCGAGCC 300
OY	354 TTCTCTTTCACCTTGTGTCAAGAATGTCCTCTGGGGTGTGATGTGCTATGAT 413
Db	301 TTCTCTTTCACCTTGTGTCAAGAATGTCCTCTGGGGTGTGATGTGCTATGAT 360
OY	414 CTGTACGGCCATCTGCCACCCCCCTCGATATTGGCATCATGACCTGGAGAGTC 473
Db	361 CTGTACGGCCATCTGCCACCCCCCTCGATATTGGCATCATGACCTGGAGAGTC 420
OY	474 ATCACCTCGGGTGAATTCTGGGACACTGGAGTCTTATCTGTGATCTGTG 533
Db	421 ATCACCTCGGGTGAATTCTGGGACACTGGAGTCTTATCTGTGATCTGTG 480
OY	534 TTACTCTACCTTACCCCTGTAGGCCCCAGAAATTACTTTTTGGAAT 593
Db	481 TTACTCTACCTTACCCCTGTAGGCCCCAGAAATTATCAC-TTTTTGGAAT 539
OY	594 CTGGCTGTCTCAAACCTGGCTGTGAGATAACCACTCAATGAGAACATGGCTTGCC 653
Db	540 CTGGCTGTCTCAAACCTGGCTGTGAGATAACCACTCAATGAGAACATGGCTTGCC 599
OY	654 CGGAGCAATTCTGGGCTGGGGACCCCTGTCCACATATGTTATATGTGAT 713
Db	600 CGGAGCAATTCTGGGCTGGGGACCCCTGTCCACAAATGTGATTTATGTGAT 659
OY	714 CCTCTGTGCTATCCTCAAGATCCATCAAGGGAAAGTCAAGGAAGGCTTCGACCTG 773
Db	660 CCTCTGTGCTATCCTCAAGATCCATCAAGGGAAAGGCTTCGACCTG 719
OY	774 CTCTCCCACCTCTGTGTGATGGACTCTTTATGGCACACCCATTATCATGTATGTGG 833
Db	720 CTCTCCCACCTCTGTGTGATGGACTCTTTATGGCACACCCATTATCATGTATGTGG 779
OY	834 ACCCAGATATGGGACCCCAAGGACCAAGAATACTCTCTGTGTTCACGCCCT 893
Db	780 ACCCAGATATGGGACCCCAAGGACCAAGAATACTCTCTGTGTTCACGCCCT 839
OY	894 TATCCATGTCATCCCTTATCTGTAGTCTTAGGACTCCAGAAGTGAAGAATCTT 953
Db	840 TATCCATGTCATCCCTTATCTGTAGTCTTAGGACTCCAGAAGTGAAGAATCTT 899
OY	954 GAAGAGAGTCTGGGAGTAGAAGGGCTTATGA 987
Db	900 GAAGAGAGTCTGGGAGTAGAAGGGCTTATGA 933
XX	AAH31617 standard; DNA; 930 BP.
SQ	Sequence 930 BP; 193 A; 265 C; 202 G; 270 T; 0 other;
Query Match	88.8%; Score 900.6; DB 22; Length 930;
Best Local Similarity	99.4%; Pred. No. 5.9e-260;
Matches	925; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY	55 ATGGGGACAAATAACATCCATCACAGAGTTCTCTACTGGGATTCCCGRTGGCCA 114
Db	1 ATGGGAGACAATAACATCCATCACAGAGAGTTCTCTACTGGGATTCCCGRTGGCCA 60
OY	115 AGGATCAGATGCTCTCTTGGCTCTCCCGTCTACGCTTACCCGTGGG 174
Db	61 AGGATCAGATGCTCTCTTGGCTCTCCCGTCTACGCTTACCCGTGGG 120
OY	175 AACGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCC-TGTACTTC 233
Db	121 AACGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCCATGTACTTC 180
OY	234 TTCTCTCACACCTGGGGCTGTCGACATCGCCTACGCTGCAACACGGTCCCCGGATG 293
Db	181 TTCTCTCACACCTGGGGCTGTCGACATCGCCTACGCTGCAACACGGTCCCCGGATG 240

QY	294	CTGGTGAACTCCTGCATCCAGCCAAGCCATCTCCTTGGGGCCATGATGCCACC	353	XX	(DIGI-) DIGISCENTS.
PA	241	CTGGTGAACCTCCTGCATCCAGCCAAGCCATCTCCTTGGGGCCATGATGCCACC	300	XX	(YEDA ) YEDA RES & DEV CO LTD.
QY	354	TTCTCTGTTTCACTTGTGTCACAGAATGTCCTCTGGGGATGTCATGTC	413	XX	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
DB	301	TTCTCTGTTTCACTTGTGTCACAGAATGTCCTCTGGGGATGTCATGTC	360	DR	WPI; 2001-290713/30.
QY	414	CTGTACGGCATCTGCCACCCCTCGATATTGGCATCATGACCTGGAGACTG	473	XX	New polynucleotides which encode polypeptides involved in olfactory
DB	361	CTGTACGGCATCTGCCACCCCTCGATATTGGCATCATGACCTGGAGACTG	420	PS	sensation for identifying olfactory agonists and antagonists -
QY	474	ATCACCCCTCGGGTACTTCCTGGACCACTGGAGTCCCTTGTC	533	XX	Claim 8; Page 264-265; 1857pp; English.
DB	421	ATCACCCCTCGGGTACTTCCTGGACCACTGGAGTCCCTTGTC	420	PT	PT
QY	534	TTACTTCTACCTTACCCCTCTGTAGGCCACCCCTCGATATTGGCAT	593	XX	XX
DB	481	TTACTTCTACCTTACCCCTCTGTAGGCCACCCCTCGATATTGGCAT	539	XX	XX
QY	594	CTTGGCTGTCTCAACTTGCCATTGCGACACTGGAGTCCCTTATG	653	XX	XX
DB	540	CTTGGCTGTCTCAAACTTGCCATTGCGACACTGGAGTCCCTTATG	599	CC	The present sequence is one of a number of isolated polynucleotides
QY	654	CGGAGCAATTCTGGCTGGACCCCTGTCACAAATTGAGTTCAT	713	CC	which encode polypeptides involved in olfactory sensation. The
DB	600	CGGAGCAATTCTGGCTGGACCCCTGTCACAAATTGAGTTCAT	659	CC	polynucleotides can be used in screening for olfactory agonists and
QY	714	CCTCTGTGCTATCCTCAGATCCAATCAAGGAAAGTCAGAGGAA	773	CC	antagonists. The methods allow for the determination of primary
DB	660	CCTCTGTGCTATCCTCAGATCCAATCAAGGAAAGTCAGAGGAA	719	CC	scents and the identification of the odour receptors used to detect
QY	774	CTTCTCCACCTCTGTGTGATTGGACTCTTATGCCACAGCCATT	833	CC	these primary scents. The methods also enable determination of
DB	720	CTTCTCCACCTCTGTGTGATTGGACTCTTATGCCACAGCCATT	779	CC	secondary scents and the identification of combinations of odour
QY	834	ACCCAGATATGGAAACCCAAAGGAGCAGAAGAATATCTCC	893	CC	receptors that are involved in detecting such secondary scents.
DB	780	ACCCAGATATGGAAACCCAAAGGAGCAGAAGAATATCTCC	839	CC	This enables the construction of a scent representation (also called
QY	894	TATCCATGCTCAATCCCTATCTGTAGTCTTAGGAACCTGAGT	953	CC	a scent fingerprint or scent profile), which may be used to re-create
DB	840	TATCCATGCTCAATCCCTATCTGTAGTCTTAGGAACCTGAGT	899	CC	and determining the interaction pattern of a composition with the receptors
QY	954	GAAGAGAGTGTGGAGTAGAAAGGGCTTA	984	CC	and can be used for determining differences in the olfactory
DB	900	GAAGAGAGTGTGGAGTAGAAAGGGCTTA	930	CC	faculties
RESULT 9				CC	of different individuals.
AAH31648				XX	
ID	AAH31648	standard; DNA; 930 BP.		XX	Sequence 930 BP; 193 A; 265 C; 202 G; 270 T; 0 other;
XX				XX	
AC	AAH31648;			XX	Query Match
XX				XX	Best Local Similarity
DT	30 - JUL - 2001 (first entry)			XX	Score 900.6; DB 22; Length 930;
XX				XX	Matches 925; Conservative 0; Mismatches 4; Indels 2; Gaps
QY	55	ATGGGGACAATAACATCCATCACAGAGTCTCTACTGGATTCCCGTGGCCA	114	XX	
DB	1	ATGGGGACAATAACATCCATCACAGAGTCTCTACTGGATTCCCGTGGCCA	60	XX	
QY	115	AGGATTCAGATGCTCTTGGGCTCTCCTCTGTCTACGGCTTCACCCGTGGGG	174	XX	
DB	61	AGGATTCAGATGCTCTTGGGCTCTCCTGTCTACGGCTTCACCCGTGGGG	120	XX	
QY	175	AACGGGACCATCTGGGCTCATCTCACTGGACTCCAGACTGCCACCCCC-TGTACTTC	233	XX	
DB	121	AACGGGACCATCTGGGCTCATCTCACTGGACTCCAGACTGCCACCCCCATGTACTTC	180	XX	
QY	234	TCCTCTCACACCTGGGGTGTGACATGCCACACGGGGGGATG	293	XX	
DB	181	TCCTCTCACACCTGGGGTGTGACATGCCACACGGGGGGATG	240	XX	
QY	294	CTGCTGAACCTCCTGCATCCAGCCAGCCATCTCCTTGCGACATGCCACACGGGGGGATG	353	XX	
DB	241	CTGCTGAACCTCCTGCATCCAGCCAGCCATCTCCTTGCGACATGCCACACGGGGGGATG	300	XX	
QY	354	TTCTCTGTTCACTTGTGTCACAGAATGTCCTCTGGGGATGTCATG	413	XX	
DB	301	TTCTCTGTTCACTTGTGTCACAGAATGTCCTCTGGGGATGTCATG	360	XX	
QY	414	CTGTACGGCATCTGCCACCCCTCGATATTGGCATCATGACCTGGAGACTG	473	XX	
DB	361	CTGTACGGCATCTGCCACCCCTCGATATTGGCATCATGACCTGGAGACTG	420	XX	
QY	474	ATCACCCCTCGGGTACTTCCTGGACCACTGGAGTCCCTTGTC	533	XX	
DB	421	ATCACCCCTCGGGTACTTCCTGGACCACTGGAGTCCCTTGTC	480	XX	
PN	W0200127158-A2.			XX	
XX	19 - APR - 2001.			XX	
PD	06 - OCT - 2000; 2000WO-0S27582.			XX	
PR	08 - OCT - 1999; 99US-0158615.			XX	
PR	24 - FEB - 2000; 2000US-0184809.			XX	



Db 294 CCATCATCATGATGCCCAACTCCGCCATCTGAGGAGCAGCAAAGGCTTT 235  
 QY 875 TGCTGTTCACAGCCTTAAATCCATGCTCAATCCCTTATCTGAGTCTTAGGAAC 934  
 Db 234 TCTTATTTACAGTTTCAACCTTAACCCCTGATTACGCCTGAGGAACG 175  
 QY 935 CAGAAGTGAAGATACTTGAGAGAGTGTGGAGTAGAAAGGCTTATGA 987  
 Db 174 GAGAGGTCAAGGGTGCCTGAGGAGACTGGCAAGGAAGTCATTCTAA 122  
 RESULT 11  
 ABA55696/C  
 ID ABA55696 standard; DNA; 1957 BP.  
 XX  
 AC ABA55696;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX Human foetal liver single exon nucleic acid probe; ss.  
 XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX Homo sapiens.  
 PN XX  
 PD XX  
 XX 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR XX  
 PT WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver.  
 PS XX  
 Claim 1: SEO ID NO 4001; 639pp + sequence listing; English.  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a single exon nucleic acid  
 CC probe of the invention.  
 Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).  
 XX  
 SQ Sequence 1957 BP; 604 A; 368 C; 495 G; 490 T; 0 other;  
 Query Match 53.7%; Score 545; DB 22; Length 1957;  
 Best Local Similarity 74.6%; Pred. No. 6e-153;  
 Matches 711; Conservative 0; Mismatches 240; Indels 2; Gaps 2;  
 QY 36 TTCCCTCTGTCATAGGGATATGGGGACAATAACATCCATCACAGAGTCTCTACT 95  
 Db 1073 TTTCTTTTACAGGAAATGGGGAAATCAGACATGGTCACAGAGTCTCTACT 1014  
 QY 96 GGGATTCCGTCAGGATTCAGATGCCCTTGGCTCTCCCTGTC 155  
 Db 1013 GGGATTCTCTGGGCCAAGGATTCAGATGCTCTTGGCTCTCCCTGTC 954

Db 833 CAACACGGTCCCCGATGCTGGTGAAACCTCTGCAATCCAGGCCAAGCCCATCTCTTGC 334  
 QY 335 GGGCCGATGATGCAGACCTTCGTTCCACTTTGCTGTACAGAATGTCCTCC 394  
 Db 773 TGGTGGCATGACGCCAGCTTCTCTGTTGAGTTTGACACAGCGNATGTCCTG 714  
 QY 395 GGTGGTGTGCTCATGATGTCAGTGTGGCCATCTGCCACCCCTCGATATTGGCCAT 454  
 Db 713 GGTGCTGATGTCCTACGATGTTACGTTGCTTACGTTGCCATCTGCCACCTCTCCGATACTCCGTCA 654  
 QY 455 CATGACCTGGAGACTGTCGATCACCCCTGGGTGACTTCTGACCACTGGAGTCTTT 514  
 Db 593 GCCTCTGGCCATGGGGTCTCATCCTAACGACTGCCCCATCTGGGCTCATGAAATCAA 534  
 XX  
 QY 575 TCACTTTTTGTAATCTTGGCTGTTACCTTACCCCTGTCAGATACCCATCA 634  
 Db 533 CCAC-TCCTCTGTGAATCCTGTCCTCAGGCTGGCTGACACCTGGCTCA 475  
 QY 635 ATGAGAACATGGCTGGGGAGCAATTCTGGCTGGGGACCCCTGTCACAATTG 694  
 Db 474 ACCAGGTGGTCATCTTGCAGCCTGCGTGTCTCTGGGGCCACCCAGCCTGGTGC 415  
 QY 695 TAGTTCATATAATGTCATCCTCTGTGCTATCCTTCAGATCCAAATCAAGGGAAAGTTCAGA 754  
 Db 414 TTGTCTCTACTGCACATCTGGGGCCATCTGGGAGTCAGCTGGGGCCCA 355  
 QY 755 GGAAGCCTCTGCCACCTGCTTCTCCACCTCTGTGATGGACTCTTATGGCACAG 814  
 Db 354 GAAAGGCCCTCTCCACCTGCTTCTCCACCTCTGGGGAGCTCTTGGCAGTG 295  
 QY 815 CCATTATCATGATGTTGGACCCAGATGGAAACCCCAAGGGAGCAGAAAGGATATCTCC 874  
 Db 294 CCATCATCATGTCATGGCCCCAACCTCCGCCATCTGAGGAGCAGCAAAGGCTTT 235  
 QY 875 TGCTGTTCACAGCCTTAAATCCATGCTCAATCCCTATCTGAGTCTTAGGAAC 934  
 Db 234 TTCTTATTTACAGTTTCAACCCACACTTAACCCCTGATTCAGCTGGAGAAGC 175  
 QY 935 CAGAAGTGAAGATACTTGAGAGAGTGTGGAGTAGAAAGGCTTATGA 987  
 Db 174 GAGAGGTCAAGGGTGCCTGAGGAGGACTGGCAAGGAAGTCATTCTAA 122  
 RESULT 12  
 AAI13969/C  
 ID AAI13969 standard; DNA; 1957 BP.  
 XX  
 AC AAI13969;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Probe #3902 for gene expression analysis in human cervical cell sample.  
 XX  
 KW Probe; human; microarray; gene expression; cervical epithelial cell;  
 cervical cancer; ss.  
 XX  
 OS Homo sapiens.

PN WO200157278-A2.

XX

PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

PF 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488901/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -

XX Claim 25; SEQ ID No 3902; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes (SENPs). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX Sequence 1957 BP; 604 A; 368 C; 495 G; 490 T; 0 other;

QY Query Match 53.7%; Score 545; DB 22; Length 1957;

Best Local Similarity 74.6%; Pred. No. 6e-153;

Matches 711; Conservative 0; Mismatches 240; Indels 2; Gaps 2;

Db 1073 TTTCTCTTCACAGGAAATGGGGAAATACATCCATCACAGAGTTCCTCCACT 95

QY 96 GGGATTCCCGTGGCCAAAGGATCAGATGCCCTTGGCTCTTCTCCGTCTA 155

Db 1013 GGGATTCTCCCTGGGCCAAAGGATCAGATGCCCTTGGCTCTTCTCCGTCTA 954

QY 156 CGTCTTCACCCCTGCTGGGAACGGGACCATCTGGGCTCATCTCACTGGACTCCAGCT 215

Db 953 TATCTTCACCCCTGCTGGGAACGGGCCATCTGGGCTCATCTCACTGGACTCCAGCT 894

QY 216 GCACGCCCUU-TGTACTTCTTCCCTCACACCTGGGGCTGACATCGCTACGCCCTG 274

Db 893 CCACACCCCCATGACTCTTCTCACACCTGGCTGTCGACATCGCTACACCCG 834

QY 275 CAACACGGGCCACATGCTGGGAACCTCTGGCTCATCCAGCCAAAGCCATCTCTTG 334

Db 833 CAACACGGGCCACATGCTGGGAACCTCTGGCTCATCCAGCCAAAGCCATCTCTTG 774

QY 335 GGGCCGCAATGCAACCTTCTGGCTGACAGAATGTCCTCC 394

Db 773 TGGTTGCAATGACGACCTTCTCTGTTGAGTTGAGCTGCTG 714

QY 395 GGTGGTGAATGTCATCTGTAACGGCCATCTGCCACCCCTCCGATATTGGCCAT 454

Db 713 GGTGCTGATGTCCTACGATCGTTACGGCCATCTGCCACCCCTCCGATACTCCGTCTA 654

QY 455 CATGACCTGGAGACTCTGCACTCACCTCGGGTGACTTCTGGACACACTGGAGTCCTTT 514

Db 653 CATGACCTGGAGACTCTGCACTCACCCCTGGCCACTTCTGGACGGCTGGCTCCCT 594

QY 515 ATCCTTGATCATTGTTACTTCTACCTTCTGTAAGGCCAGAAATTAA 574

Db 593 GCCTCTGGCCATGGTCTCATCTAAGCTGCCCTCTGGGCTCTGAAATCAA 534

QY 575 TCACTTTTGTGAATCTTGGCTGTCCTCAACTTGGCTGTCAGATACCCACATCA 634

Db 533 CCAC-TCTCTGTGAATCTCTGCTCTGGCTGGCCCTGGCTCA 475

QY 635 ATGAGAACATGCTTGGCCGGAGCAATTCTGGGCTGGGGACCCCTGCCACAATG 694

Db 474 ACCAGGTGGTCATCTTGGCAGGCTGGTGTCTCTGGGGGCCACCGCTGGTC 415

QY 695 TAGTTCATATAGTCATCCCTGCTGCTTACATCCATCACAGAACATCCAGTCAG 754

Db 414 TTGTCCTCTACTCGCACATCCCTGGGGCCATCTGAGGATCCAGTGGCACAG 814

QY 755 GAAAGCCTTCTCACCTGCTCTCCACCTCTGGTGTGATGGACTCTTATGGCACAG 814

Db 354 GAAAGCCTTCTCACCTGCTCTCCACCTCTGGTGTGGACTCTTGGCAGTG 295

QY 815 CCATATTATGATGATGGGACCCAGATGGGARCCCCAAGGGCAGAACATCTCC 874

Db 294 CCATCATCATGATGATGGGCCCAAGTCGGCCATCTGAGGAGCAGCAAAGGTCTT 235

QY 875 TGCTGTTTCACAGCCTCTTAACTCCATGCTCAATCCCTTATCTGTAGTCTAGGAAC 934

Db 234 TTCTATTTAGCACTTTCACCCACACTTAACCCCTGATTTACAGCCTGAGGAAC 175

QY 935 CAGAAGTGAAGATACTTGAGAGACTGCTGGGAGTAGAAGGGTTATGA 987

Db 174 GAGAGGTCAAGGGTGCCTGAGGAGGACTGGCAAGGAAGTCATTCTAA 122

RESULT 13

AAI35352/C

ID AAI35352 standard; DNA; 1957 BP.

XX AC AAI35352;

XX DT 17-OCT-2001 (first entry)

XX DE Probe #4038 used to measure gene expression in human placenta sample.

XX KW Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

XX PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX DR WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -

XX Claim 25; SEQ ID NO 4038; 654pp; English.

XX  
 CC The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders.  
 XX Sequence 1957 BP; 604 A; 368 C; 495 G; 490 T; 0 other;  
 Query Match 53.7%; Score 545; DB 22; Length 1957;  
 Best Local Similarity 74.6%; Pred. No. 6e-153;  
 Matches 711; Conservative 0; Mismatches 240; Indels 2; Gaps 2;  
 QY 36 TTTCTCTGTGTCATAGGGATATGGGGACAATAACATCAGACAGAGTCCTCTACT 95  
 Db 1073 TTTTCTTPTTCACAGGAAATGGGGAAATCAGACAATGGTCACAGAGTCCTCTACT 1014  
 QY 96 GGGATTCCCGTGGCCAAGGATTCAGATGCCTCTTGGCTCTCCCTGTCTA 155  
 Db 1013 GGGATTCTCTCTGGGCCAAGGATTCAGATGCCTCTTGGCTCTCCCTGTCTA 954  
 QY 156 CGTCTCACCCGTGGGAAACGGGACATACTGGGCTCATCTACTGGACTCAGACT 215  
 Db 953 TATCTCACCCGTGGGAAACGGGACATCCGGGCTCATCTACTGGACTCAGACT 894  
 QY 216 GCACGCCCGG-TGTACTCTTCCTCTCACACTGGGGCTGTCACATGCCTACGGCTG 274  
 Db 893 CCACACCCCCATGTACTTCCTCTCACACCTGGCTGTCGACATGCCTACACCCG 834  
 QY 275 CAACACGGTGCCCGGATGCTGGTAACCTCCGCATCCAGCCACATCTCCCTTG 334  
 Db 833 CAACACGGTGCCCGAGATGCTGGGAACCTCCGCATCCAGCCACATCTCCCTTG 774  
 QY 335 GGGCCGATGAGCAGACCTTCGTTTCCACCTTGCTGTCACAGAATGTCCTCT 394  
 Db 773 TGGTTGCACTGACGCAGACCTTCTCTGTTGAGTTGGACACAGGAAATGTCCTG 714  
 QY 395 GGGGGTGTGATGCTCATGATCTGTAAGTGGCCATCTGCCACCCCCCTGGATATTGGCCAT 454  
 Db 713 GGTGCTGATGTCCTACGATCGTTACGTGGCCATCTGCCACACCTCTCGATCAT 654  
 QY 455 CATGACCTGGAGAGTCGCATCACCCCTGGGGTGAETCTGGGACACTGGAGTCCTT 514  
 Db 653 CATGACCTGGAGAGTCGCATCACCCCTGGGGTGAETCTGGGACACTGGAGTCCTT 594  
 QY 515 ATCCTTGATTCATCTGGTACTCTACCTTACCTTCTGAGGCCAGAAATTAA 574  
 Db 593 GCTCTGGCCATGTTGAAATCCCTGTCACCTGGCTGGCTGTCGAGACACTGGCTCA 534  
 QY 575 TCACTTTTGTGAATCTGGCTGTCACAATCTGGCTGTCAGA 634  
 Db 533 CCAC-TCTCTGTCACCTGGCTGGCTGTCGAGACACTGGCTCA 475  
 QY 635 ATGAGAACATGGTCTGGGGAGCAATTCTGGCTGGGGACCTTGCCACAATTG 594  
 Db 474 ACCAGGGTCATCTTGCAGCCTGGCTGTCCTGGGGCAACCCAGCCGGCTGGTC 415  
 QY 695 TAGTTCATATATGGCATCTCTGGCTATCTTCAGATCCAACTCAAGGAAGTCAGA 754  
 Db 414 TGTCTCTACTGGCACATCTGGGGCAACCCAGCCGGCTGGTC 355  
 QY 755 GGAAGGCTCTGGACCTCTCCACCTCTGGTGTGATGGACTTTATGGCACAG 814  
 Db 354 GAAAGGCTCTCCACCTGCTCCACCTGGGGACTCTGGCTGGAGTCAGTCAGTG 295  
 QY 815 CCATTATCATGATGTTGGACCCAGATATGGAAACCCAGGGCAGAAATATCTCC 874  
 Db 294 CCATCATCATGATGTCAGGGCCATCTGGAGGAGCAAGGCTT 235  
 QY 875 TGTGTTCACAGCCTTAATCCCATGCTCAATCCCTTATCTGAGTCAGTCAGGAACT 934  
 Db 234 TCTTATTTCAGGTTCAACCAACTAACCCCTGATTACAGCCTGAGGAACG 175

QY 935 CAGAAGTGAAGATACTTGAAGAGAGTGCTGGGAGTAGAAAGGGCTTATGA 987  
 ID ABS03949/C  
 ID ABS03949 standard; DNA; 1957 BP.  
 XX RESULT 14  
 ID ABS03949/C  
 ID ABS03949 standard; DNA; 1957 BP.  
 XX AC  
 XX DT 19-AUG-2002 (first entry)  
 XX DE Human genome-derived single exon probe from lung SEQ ID No 3940.  
 XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangiomatosis; Karagener syndrome;  
 KW primary cilial dyskinesia; fibrocystic pulmonary dysplasia;  
 KW hyaline membrane disease.  
 XX OS Homo sapiens.  
 XX PN WO200186003-A2.  
 XX PD 15-NOV-2001.  
 XX PR 30-JAN-2001; 2001WO-US00665.  
 XX PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2002-114183/15.  
 XX PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 XX PS Claim 1; SEQ ID NO 3940; 634PP; English.  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of

expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <ftp://wipo.int/pub/published/pct/sequences>.

SQ Sequence 1957 BP; 604 A; 368 C; 495 G; 490 T; 0 other;

Query Match 53.7%; Score 545; DB 24; Length 1957;  
 Best Local Similarity 74.6%; Pred. NO. 6e-153;

QY 36 TTTCCCTCTGTCA TAGGATATGGGGACAATAACATCCATCACAGAGTTCCCTCCTACT 95  
Matches 7/11; Conservative 0; Mismatches 240; Indels 2; Gaps 2;

Db 1073 TTTCTTTTCACAGGAAATGGGAAATCAGACAAATGGTCACAGAGTTCCCTCCTACT 1014

oy	96	GGGATTCCCGTGGCCAAGGATTCAGATGCTCTTGGCTCTCCCTGTTCA	155
bb	1013	GGGATTCTCCTGGCCAAGGATTCAGATGCTCTTGGCTCTCCCTGTTCA	954

QY 156 CGTCTCACCTGCTGGGAACGGACCATACTGGGCTCATCTCACTGGACTCCAGACT 215

QY 275 CAACACGGTCCCCGGATGCTGGTGAACCTCCTGCATCCAGCCAAAGCCATCTCCTTTC 334

QY bb 833 GGGCCGCATGATGCAGACCTTCTGTTCACTTGTGTCACAGAATGTCCTCCT 394

DB 773 TGGTTGCATGACGCCAGACCTTCTCTGTTGAGTTGGACACAGCGAATGTCCTGCT 714

QY	395	GTTGGTGTATGATCTGTACGGGCCATCTGCCACCCCTCCGATATTGGCCAT	454
Bb	713	GTTGCTGATGTCCTACGATCTTACGTCGCGATCTGGGACCGCTTCCGATCTGCT	651

QY 455 CATGACCTGGAGAGTCTGCATCACCTCGGGTCACTTCTGGACCACTGGAGTCCTTT 514

Db 653 CATGACCTGGAGAGTCTGCATCACCTGGCGTCACCTGGACGTTGGCTCCCTCCT 594

Db	593	GGCTCTGCCCATGGTCTCATCTTAAGACTGCCCTCTGGCCTCATGAATCAA	534
dy	515	ATCCCTGATTCATCTGGTTACCTCTACCTTACCTCTCTCTCTAGGCCCCAGAAATT	574

QY 575 TCACTTTTTGTGAATCTGGCTGTCACACTGCCTGTCAGATAACCCACATCA 634

DB 533 CCAC - TTCTTCTGTGAATCCTGTCGTGCTCAGGCCCTGTGCTGACACCTGGCTCA 475  
8V 635 ATGAGAACATGGCTTGGGGAGCAATTCTGGCTGGACCC'TTGTCCACAATTG 694

Db 474 ACCAGGTGGTCATCTTGCAGCCTCGGTGTCCTCCGGTGGGCCACCCAGCCTGGTGC 415

695 TAGTTCATATATGTCATCCTCTGTGCTATCCTCAGATCCATCAAGGGAGTCAGA 754

BB 414 TGGCTTACGGCAATGGGGGATCCAGGGATCAGCTGGGAGGGCGCA 355

QY 755 GGAACCTCTGCACCTCTCCACCTCTGTTATGGCACAG 814  
 | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 354 GAAAGGCCTCTCCACCTGCTCCACCTCTGGTGGACTCTCTTGGCAGTG 295  
 QY 815 CCATTATCATGATGTTGACCCAGATGGAACCCAAAGGAGCAGAAATATCTCC 874  
 | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 294 CCATCATCATGATGGCCCCAACGTCCGCCATCTGAGGAGCAGCAAAGGTCTTT 235  
 QY 875 TGCTGTTCACAGCCTTTAATCCATGCTCAATCCCTATCTGTTAGTCTAGGAACR 934  
 | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 234 TTCTATTTACAGTTTCAACCCAAACCTTAACCCCTGATTACAGCCTGAGGAACG 175  
 QY 935 CAGAAGTGAAGATACTTGAAGAGAGTGGGGAGTAGAAAGGGCTTATGA 987  
 | ||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 174 GAGAGGTCAAGGGTGCCTGAGGAGCACTGGCAAGGAAGTCAATTCTAA 122

RESULT 15

AAS08660  
 ID AAS08660 standard; cDNA; 2282 BP.  
 XX  
 AC AAS08660;  
 XX  
 DT 17-DEC-2001 (first entry)

XX Human cDNA encoding G-protein coupled receptor like protein, GPCR #13.  
 DE Human; G-protein coupled receptor like protein; GPCR; immunogen;  
 KW ophthalmic disease; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; HIV; candidiasis;  
 KW human immunodeficiency virus; autoimmune disorder; multiple sclerosis;  
 KW systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;  
 KW thrombocytopaenia; aplastic anaemia; inflammatory disorder;  
 KW septic shock; systemic inflammatory response syndrome; SIRS;  
 KW hormonal dysfunction; cancer; atherosclerosis; wound;  
 KW tissue regeneration; haemophilia; leukaemia; reperfusion injury;  
 KW psoriasis; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 KEY Location/Qualifiers  
 FH 1257..2189  
 FT /\*tag- a  
 FT /product= "GPCR #13"  
 XX  
 PN WO200153454-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-US34983.  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 20-JUN-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 31-AUG-2000; 2000US-0653450.  
 PR 04-DEC-2000; 2000US-0729739.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F;  
 PI Asundi V, Drmanac RT;  
 XX  
 DR WPI; 2001-442255/47.  
 DR P-PSDB; AAU04582.  
 XX  
 PT New G-protein-coupled receptor-like polypeptides and polynucleotides,  
 PT useful for treating diseases of ophthalmic, neurological, immunological,  
 PT and nephritic systems and hormonal dysfunction, cancer, atherosclerosis  
 PT and diabetes -  
 XX  
 PS Claim 1; Page 256-25B; 259pp; English.

XX  
 CC The sequence encodes a human G-protein coupled receptor (GPCR)-like  
 CC protein. The GPCR-like polypeptides and polynucleotides are useful for  
 CC the treatment of diseases of ophthalmic, neurological (e.g Alzheimer's  
 CC disease and Parkinson's disease, immunological (e.g HIV infection and  
 CC candidiasis), autoimmune disorders (e.g multiple sclerosis, systemic  
 CC lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g.  
 CC thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g.  
 CC septic shock and systemic inflammatory response syndrome, SIRS) and  
 CC nephritic systems. They may also be used to treat hormonal dysfunction,  
 CC cancer, atherosclerosis, wounds, tissue regeneration, haemophilia,  
 CC leukaemias, reperfusion injury, psoriasis and diabetes. Numerous examples  
 CC of each type of disorder are given in the specification. Anti-GPCR-like  
 CC protein antibodies are useful for detecting or quantitating the  
 CC polypeptide in tissue. The polypeptides can also be used as molecular  
 CC weight markers and as a food supplement.  
 XX  
 SQ Sequence 2282 BP; 583 A; 573 C; 428 G; 698 T; 0 other;

Query Match 53.1%; Score 538.2; DB 22; Length 2282;  
 Best Local Similarity 73.6%; Pred. No. 7.2e-151; Mismatches 253; Indels 2; Gaps 2;  
 Matches 712; Conservative 0; Mismatches 253; Indels 2; Gaps 2;

Qy 31 CTTGAGATTCTCTCTGTCATAGGGATATGGGGACAATAACATCCATCACAGAGTTCTC 90  
 Db 1233 CTTTGTGTTGTTTTAGTAGTGAATGGTAAATGGTAAAGACAATGGTCACAGAGTTCTC 1292

Qy 91 CTACTGGGATTCCCGTGGCCCAAGGATTCAGATGCTCTCTTGCCCTCTCTCCTG 150  
 Db 1293 CTACTGGGATTCTCTGGCCCAAGGATTCAGATGCTCTCTTGCCCTCTCTCCTG 1352

Qy 151 TTCTACGTTTACCCCTGCTGGGGAAAGGACCATCTGGGCTCATCTCACTGGACTCC 210  
 Db 1353 TTCTATGCTTACCCCTGCTGGGGAAAGGACCATCTGGGCTCATCTCACTGGACTCC 1412

Qy 211 AGACTGCACGGCCCC -TGTACTTCTCTCACACCTGGGGCTGAGCATGGCTC 269  
 Db 1413 AGACTCCACACCCCCATGTACTTCTCTCACACCTGGGGCTGAGCATGGCTC 1472

Qy 270 GCCTGCAACACGGTCCCCGATGATGCAGACCTTCTGCACTCCAGCAAGGCCATCTC 329  
 Db 1473 GCCTGCAACACAGTGCAGATGCTGGGAACCTCTGCATCCAGCAAGGCCATCTC 1532

Qy 330 TTGCGGGCCGCATGATGCAGACCTTCTGTTCACTTGTGCACTCCAGCAAGGCCATCTC 389  
 Db 1593 TTGCGGGCTGATGTCTACGATGGCTGACAGACCTTCTCCTTTGAGTTTGCACTACTGAAATGCC 1652

Qy 450 GCCATCATGGACCTGGAGAGTCTGCATCACCTGGGACACTGGAGTC 509  
 Db 1653 ATCATCATGGACCTGGAAAGTCTGCATCACCTGGGACACTGGAGTC 509

Qy 510 CTTTATCCCTGATTCTACCTTGTTACTCTACCTTACCCCTCTGTAGGCCAGAA 569  
 Db 1713 CTCCCTGGCTATGGCCATGTGAGCTCATCTAACACTGGCCCTTGTCATGGCTGAA 1772

Qy 570 ATTATCACTTTTGTGAATCTGGCTCTGCTCAACTTGCCCTGGACCTGGCC 629  
 Db 1773 ATCAACACAC-TTCTCTGTAATCTGGCTGAAATCTGGCTCTGCTCAACTTGCCCTGGACCTGGCC 629

Qy 630 CATCAATGAGAACATGTGCTGGCGGAGCAATTCTGGCTGGACCTGGCC 689  
 Db 1832 GCTCAACAGGTCGTCATCTTGAGCTGATGTCATCTGGGACACTGGCTC 1891

Qy 690 ATTTGAGTTCTCATATATGTGCATCCTCTGCTCAAGGAAAGT 749  
 Db 1892 GGTGCTGGCTCTGACTCACACATCTGGGGCATCTGGAGATCCAGTCTGGGGAGGG 1951

Qy 750 TCAGAGGAAGCCTCTGCACCTGCTCTCCACCTCTGTGTGATGGACTTTATGG 809

Db 1952 CGCAGAAAGGCCTCTCCACCTGCTCTCCACCTCTGGTAGTGGGACTCTCTTGG 2011  
 Qy 810 CACAGCATTATCATGATGTTGGACCCAGATATGGAAACCCAGGGAGAAATA 869  
 Db 2012 CAGGCCATCGTCATGTCATGGCCCTAAGTCCCCTGAGGAGCAGCAGAAGGT 2071  
 Qy 870 TCTCCCTGCTGTTCACGCCCTTAATCCATGCTCAATCCCTATCTGTAGTC 929  
 Db 2072 CCTTTTCTATTACAGTCTTCAACCCGATGCTAAACCCCTGATTACACCTGAG 2131  
 Qy 930 GAACCTAGAAGTGAAGAATCTTGAGAGAGTGTGGAGTAGAAAGGGCTTATGAA 989  
 Db 2132 GAATCTAGAGGGTCAAGGGTGGCCCTGAGGAGAGCACTGTGCAAGGAAAGTCATTCTAAGA 2191  
 Qy 990 AGGATA 996  
 Db 2192 GGTGAGA 2198

Db 1952 CGCAGAAAGGCCTCTCCACCTGCTCTCCACCTCTGGTAGTGGGACTCTCTTGG 2011  
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 Job time : 293 secs



OM nucleic - nucleic search, using Sw model

Run on: May 2, 2003, 04:52:26 ; search time 1543 seconds  
(without alignments)

10643.048 Million cell updates/sec

Title: US-09-898-586-23

Perfect score: 1014

Sequence: 1 taaacacttctcctaaacca.....tatggcattgtgactgacaa 1014

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_esthun:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

7 394.8 38.9 705 11 AF327904 Homo sapi AF327904 Homo sapi  
8 394.8 38.9 751 12 BE856570 7f64e08.x BE856570 7f64e08.x  
9 380.6 37.5 738 9 AI079550 o204f08.x AI079550 o204f08.x  
10 370.4 36.5 732 12 BF116115 7n77g04.x BF116115 7n77g04.x  
11 359 35.4 580 10 BE543056 601068985 BE543056 601068985  
12 355 35.0 367 9 AI340119 qk64f08.x AI340119 qk64f08.x  
13 345.6 34.1 426 14 H62441 yr79d08.r1 H62441 yr79d08.r1  
14 345.6 34.1 623 13 BM670360 UI-E-DW1- BM670360 UI-E-DW1-  
15 337.4 33.3 361 9 AI285267 q138c08.x AI285267 q138c08.x  
16 332.6 32.8 690 10 BE179276 RC1-HT061 BE179276 RC1-HT061  
17 331 32.6 439 14 H62445 H62445 yr79e08.r1  
18 320 31.6 441 13 BT020419 BT020419  
19 305.2 30.1 499 10 AW299289 AW299289  
20 293.8 29.0 332 10 BE182734 BE182734 RC3-HT065  
21 272.4 26.9 788 17 BE11304 BE11304 RPC1-24-3  
22 267.4 26.4 432 10 BE174029 BE174029 0V1-HT057  
23 265.2 26.2 671 12 BF974217 BF974217 602243851  
24 242.8 23.9 520 17 AQ600752 HS\_5346\_B AQ600752 HS\_5346\_B  
25 232 22.9 376 12 BE926655 BE926655 OV1-BT063  
26 222.6 22.0 449 14 H39851 H39851 yp01h12.s1  
27 214.4 21.1 432 9 AA962054 AA962054 oq79901.s0  
28 211.8 20.9 760 12 BG169291 BG169291 602321020  
29 206.8 20.4 1394 11 AK017036 AK017036 Mus muscu  
30 206.8 20.4 3063 11 AK016560 AK016560 Mus muscu  
31 203 20.0 445 14 H39853 H39853 yp01h12.s1  
32 183.6 18.1 226 9 AI084964 AI084964 ov86f03.s9  
33 180 17.8 231 13 BG984943 BG984943 IL5-CN006  
34 174.4 17.2 796 12 BG197640 BG197640 RST17016  
35 174 17.2 762 12 BG193339 BG193339 RST12467  
36 173.6 17.1 495 12 BF841098 BF841098 PM8-HT035  
37 173.4 17.1 661 13 BG924888 BG924888 HNC36-1-B  
38 162.8 16.1 445 14 BM712072 BM712072 UI-E-DW1-  
39 162.4 16.0 428 14 BM707299 BM707299 UI-E-CR1-  
40 160.8 15.9 642 17 AZ969227 AZ969227 2M0241J24  
41 160.4 15.8 1501 11 AK016338 AK016338 Mus muscu  
42 160.2 15.8 732 12 BG068751 BG068751 H3068H10-  
43 156.4 15.4 786 12 BG204873 BG204873 RST24289  
44 155.6 15.3 915 14 BQ888002 BQ888002 AGENCOURT  
45 153.8 15.2 632 17 AZ765752 AZ765752 1M0562B19  
A2765752 1M0562B19

## ALIGNMENTS

RESULT 1

BC016940 BC016940

DEFINITION Homo sapiens, Similar to olfactory receptor, family 2, subfamily A, member 4, clone IMAGE:4424116, mRNA.

ACCESSION BC016940

VERSION BC016940.1

KEYWORDS HTC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 2021)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk  
Email: cgabs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	Db 1071 GTCTCCACTCACACATCCTGGGGCCATCCTGAGGATCAGCTGGGGAGCCAGA 1130
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	Qy 757 AAAGCCCTCTGCACCTGCTCTCCACCT"CTGCTGATTGGACTCTTTATGGCACAGCC 816
Series: IRAK Plate: 27 Row: 1 Column: 22	Db 1131 AAGGCCTTCTCCACCTGCTCTCCACCTCTGCGTACTGGACTCTCTTGGCAGGCC 1190
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity to protein	Qy 817 ATTATCATGTATGGACCCAGATGGGAACCCAGAGAAGANATACTCCCTG 876
This clone has the following problem: frame shifted.	Db 1191 ATCGTCATGTACATGGCCCTTAAGCCCCATCTGAGGAGCCAGAAGTCCTTTT 1250
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BASE COUNT	470 a 546 c 427 g 578 t
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Query Match	52.5%; Score 532.8; DB 11; Length 2021;
Best Local Similarity	73.5%; Pred. No. 1.9e-134;
Matches	706; Conservative 0; Mismatches 252; Indels 2; Gaps 2;
Qy 38 TCCCTCTGTCAAGGGATATGGGGACAAATACATCCATCACAGAGTTCCTCTACTGG 97	Db 412 TCATAACTATTAGTGAATAATGGTGAATAATCAGACAATGGTACAGAGTTCCTACTGG 471
Qy 98 GATTCCCGTTGCCAAGGATTAGTCAAGATGCTCCCTCTCCCTGTCTAGG 157	Db 472 GATTCTCTGGGCCAACAGATTAGTCTCCCTTTGGCTCTCTCCCTGTCTATG 531
Qy 158 TCTTCACCCCTGCTGGGACGGACATACTGGGCTCATCTACTGGACTCCAGACTGC 217	Db 532 TCTTCACCCCTGCTGGGACATCTACTGGACTCCAGACTCCAGACTOC 591
Qy 218 ACGCCCCC-TGTACTCTCTCACACCTGGGCTCGACATGGCCTACGCTTGCA 276	Db 592 ACACCCCATGTTACTTCTTCACACCTGGGGCTCATCTACTGGACTCCAGACTOC 651
Qy 277 ACACGGTCCCCGGATGCTGCTGAACCTCTCGATCCAGCCAAAGCCCATCTCTTGCGG 336	Db 652 ACACAGTGCCAGATGCTGGTGAACTCTCTGATCCAGCCAAAGCCCATCTCTTGCG 711
Qy 337 GCGCGATGATGCAGACCTTCGTGTTCACTTGCTGTCAGAGATCTCCCTCTGG 396	Db 712 GCTGCATGACATAGACCTTCCTTTGAGTTTGACACATACTGATGCAATGCCCTCTGG 771
Qy 397 TGGTGTATGTCTATGATCTGACGTGGCCATCTGCCACCCCTCCGATATTGGCCATCA 456	FEATURES
Db 772 TGCCTGATGTCTACAGATCGGTACGGTGGCCATCTGCCACCCCTCCGATATTTCATCA 831	source
Qy 457 TGAACCTGGAGAGTCTGCATCACCTCGGGTGAECTTCTGGACCACTGGAGCTTTAT 516	
Db 832 TGAACCTGGAAAGTCTCCATCACTCTGGCATCTGCACATCTGGCTCCCTGG 891	
Qy 517 CCTTGATTCATCTGGTTACTCTACCTTACCCCTCTGAGGCCAGAAATTATC 576	
Db 892 CTATGGTCCATGTGAGCCTCATCTTAAGACTGGCCCTTGTGGGGCCTCGTGAAATCAACC 951	
Qy 577 ACTTTTTTGTGAATCTGGCTCTCAAACCTGGCTGTGAGATACCCACATCAAT 636	
Db 952 AC-TCTTCTGTGAATCTGGCTCTGAGTACCTGGCTCAAC 1010	
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Best Local Similarity	99.8%; Pred. No. 3.7e-107;
Matches	443; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 637 GAGAACATGGCTGGCGGCAATTCTGGCTGGGGACCCCTGTCACAATGTA 696	Db 1011 CAGGGGGTCACTTGCAGCCTGCAATGTCATCTGGTGGGACCACTCTGCTG 1070
Qy 697 GTTTCATATGTCATCTGGCTATCCTGAGATCCAACTCAAGGGAGTCAGAG 756	Qy 143 TCTCCCTGTTCTACGTCCTCACCCCTGCTGGGGACCCATACTGGGCTCATCTCAC 202

Db	456	TCTCCCTGTTCTACGTCTCACCTGCTGGGAACGGGACATACTGGGCTCATCTCAC	397
Qy	203	TGGACTCCAGACTGCACGCCCGC-TGTACTCTCTCACACCTGGGGCGTGGACA	261
Db	396	TGGACTCCAGACTGCACGCCCGCAGTGTACTCTCTCACACCTGGGGCGTGGACA	337
Qy	262	TCGCCTACGGCTGCAACACGGTGGGGGATGCTGGTGAACCTCTGCATCCAGGAAGC	321
Db	336	TCGCCTACGGCTGCAACACGGTGGGGGATGCTGGTGAACCTCTGCATCCAGGAAGC	277
BASE COUNT	136	a 94 c 131 g 81 t 1 others	
ORIGIN			
Query Match	42.3%	Score 429.4; DB 13; Length 443;	
Best Local Similarity	99.3%	Pred. No. 1.9e-106;	
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Qy	442	GATATTGGCCATCATGACCTGGAGACTCTGCATCCACCCCTCGGACCA	501
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Qy	502	CTGGAGTCCCTTATCCTGATTCTACCTTACCCCTCGTAGGC	561
Db	96	CTGGAGTCCCTTATCCTGATTCTACCTTACCCCTCGTAGGC	37
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DEFINITION	IL5-CN0068-100401-434-d09	443 bp mRNA linear EST 12-JUN-2001	
ACCESSION	BG984967	Homo sapiens cDNA, mRNA sequence.	
VERSION	BG984967.1	GT:14387702	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 443)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Laboratory of Cancer Genetics		
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ACCESSION	BQ301355	Homo sapiens cDNA, mRNA sequence.	
VERSION	BQ301355.1	GT:2081687	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
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AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Laboratory of Cancer Genetics		
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	/clone_lib="CN0068"		

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICH Human Cancer Genome  
 Project. This entry can be seen in the following URL:  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1-HB0037-020201-589-d09&t3=2001-02-02&t4=1>)  
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 Site\_2: small; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT  
 97 a  
 120 c  
 101 g  
 138 t  
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 QY 417 TAGCTGGCCATCTGCCACCCCTCCGA-TATTTGCCATCATGACCTGGAGAGTCATGCAT 475  
 Db 4 TAGGGTGGCATCTGCCACCCCTCCGA-TATTTGCCATCATGACCTGGAGAGTCATGCAT 63  
 QY 476 CACCCCTCGGGTACTTCTGGACCTGGAGCTGGCTTTAACCTTGTATTCATCTGGT 535  
 Db 64 CACCCCTCGGGTACTTCTGGACCTGGAGCTGGCTTTAACCTTGTATTCATCTGGT 123  
 QY 536 ACTTCTACCTTAACTTCTGTAGGCCAGAAATTATCACTTTTTGTGAATCT 595  
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 QY 596 TGGCTGTCTCAAACCTGGCTGTGCAAGATAACCCACATCAATGAGAACATGGCTTGGCCG 655  
 Db 183 TGGCTGTCTCAAACCTGGCTGTGCAAGATAACCCACATCAATGAGAACATGGCTTGGCCG 242  
 QY 656 GAGCAATTCTGGCTGGGGACCCCTGGCCAAATGGTCAATATGTGCATCC 715  
 Db 243 GAGCAATTCTGGCTGGGGACCCCTGGCCAAATGGTCAATATGTGCATCC 302  
 QY 716 TCGTGTCTATCCTCAGATCCAACTAAGGAAGTCAGAGGAAGCCCTCTGCACCTGCT 775  
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 QY 776 TCTCCCACCTCTGTGATGGACTCTTATGCCACAGCCATTATCATGTATGTGGAC 835  
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 RESULT 5  
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 LOCUS A1339573 433 bp mRNA linear EST 13-FEB-1999  
 DEFINITION qk67f03.x1 NCI-CGAP\_C08 Homo sapiens cDNA clone IMAGE:1874045 3',  
 similar to SW.OLF7\_MOUSE P34984 OLFACTORY RECEPTOR-LIKE PROTEIN K7  
 ACCESSION A1339573  
 VERSION A1339573.1 GI:4076500  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 433)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapps-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
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 Seq Primer: -40UP from Gibco  
 High quality sequence stop: 411.  
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 /note="Organ: colon; Vector: pRT73D-Pac (Pharmacia) with a  
 modified polylinker; 1st strand cDNA was prepared from  
 colon adenocarcinoma, and was then primed with a Not I -  
 oligo(dt) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pRT3  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT  
 127 a  
 91 c  
 139 g  
 76 t  
 ORIGIN  
 Query Match 40.3%; Score 409; DB 9; Length 433;  
 Best Local Similarity 99.8%; Pred. No. 7.1e-101;  
 Matches 420; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Db 433 CTGCTGGAAACGGGACCATACTGGGCTCATCTCAGACTCCAGCC 225  
 QY 166 CTGCTGGAAACGGGACCATACTGGGCTCATCTCAGACTCCAGCC 374  
 Db 433 CTGCTGGAAACGGGACCATACTGGGCTCATCTCAGACTCCAGCC 374  
 QY 226 -TGTACTTCTCCCTCACACCTCTGCGGTCGTGACATGGCTACGGCTTGACAGGGT 284  
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 Db 313 CCCGGATGCTGGGAACCTCTGCATCCAGCCAAAGCCATCTCTTGGGGCCGATG 254  
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 QY 405 TCCTATGATCTGTACGTGGCCATCTGCCACCCCTCCGATATTGGCCATCTGACCTGG 464  
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 QY 465 AGAGTCTGCATCACCCCTCGGGTGACTIONGCCACTGGAGGCCTTTAACCTGTGATT 524  
 Db 133 AGAGTCTGCATCACCCCTCGGGTGACTIONGCCACTGGAGGCCTTTAACCTGTGATT 74  
 QY 525 CATCTGTGTTACTCTACCTTACCTTCTGTAGGGCCAGAAATTATCACTTTT 584  
 Db 73 CATCTGTGTTACTCTACCTTACCTTCTGTAGGGCCAGAAATTATCACTTTT 14  
 QY 585 T 585



Db	109 CTTGTTGTTAGTAGTGAATGGTGAATAATGAGTCACAGAGTCC
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Qy	151 TTCTACGCTTCACCCGCTGGGAAACGGGACATACTGGGCT
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Qy	390 CTCCTGGTGTGATGTCATGATGCTGTACGGGCCAT
Db	469 CTCCTGGTGTGATGTCATGATGCTGTACGGGCCAT
Qy	450 GCCATCATGACCTGGAGAGTCTGCATCACCC
Db	529 ATCATCATGACCTGGAAAGTCTGCATCACTT
Qy	510 CTTTATCCTGATTCTCATCTGTGTTACCTTACCC
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RESULT 8	
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DEFINITION	IMAGE:3299462 3' similar to TR:095047 095047 WUGSC:H_DJ0988615.2
ACCESSION	;
AUTHORS	;
TITLE	;
JOURNAL	;
COMMENT	;
SOURCE	human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthleria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 751) NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
CONTACT	Robert Strausberg, Ph.D.
EMAIL	cgbpls-r@mail.nih.gov
INFO	This clone is available royalty-free through LILN ; contact the IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information.
SEQ PRIMER	-40UP from Gibco
HIGH QUALITY SEQUENCE	High quality sequence stop: 449.
FEATURES	Location/Qualifiers
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RESULT 9	
LOCUS	AI079550 738 bp mRNA linear EST 29-SEP-1998
DEFINITION	OZ04f08.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674375 3' similar to SW:OLF7_MOUSE P34984 OLFACTORY RECEPTOR-LIKE PROTEIN K7 ; mRNA sequence.
ACCESSION	;
VERSION	AI079550
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

11 libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HE-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fattima Bonaldo."

BASE COUNT

170 a 206 c 137 g 238 t

ORIGIN

Query Match 38.9%; Score 394.8; DB 12; Length 751; Best Local Similarity 80.9%; Pred. No. 6.9e-97; Matches 484; Conservative 0; Mismatches 112; Indels 2; Gaps 2;

Qy 31 CTTGATTTCTGTCAAGGATATGGGACATAACATCCATCACAGAGTCC 90

Db 155 CTTTGTGTTGTTTAGTAGTGAAATGGTCAAATCAGACATGGTCAAGAGTTC 214

Qy 91 CTAUTGGGATTCCCGTGGCCAT

Db 215 CTACTGGGATTTCCTCCTGGGCGCAAGGATTCAGATGCTCTCTTGGGCTTCTCCCTG 274

Qy 151 TTCTACAGTCTCACCCGTGGGAATGGGACCATACTGGGGCTCATCTGACTCC 210

Db 275 TTCTATGTCCTCACCCGTGGGGATGGGACCATCTGGGCTCATCTGACTCC 334

Qy 211 AGACTGCACGGGG-TGTA

Db 315 AGACTCCACACCCCCATGTACTCTTCCCTCACACCTGGCCGTGCAAGATCGCTT 329

Qy 270 GCCTGCAACACGGTGGCCGATGCTGGGAACCTCTGATCCAGCCAAAGCCCATCTC 394

Db 395 GCCTGCAACACAGTGGCCCATGTGCTGGTGAACCTCTGATCCAGCCAAAGCCCATCTC 454

Qy 330 TTGGGGGGCATGATGGAGCTTCTGTTCACTTTGCTGTCAGAAATGTCTC 389

Db 455 TTGCTGGGTGATGACATAGACCTTCTCTTGTGAGTTGACATACTGAATGCC 514

Qy 390 CTCCTGGTGTGATGTCCTATGATCTGTACGTGGCCATCTGCCACCCCGTGGATATTG 449

Db 515 CTGTTGGCTGATGTCTACGATGGTACGTGGCCATCTGCCACCCCTCCGGATTTG 574

Qy 450 GCCATCATGACCTGGAGAGTCTGCATCACCCGGGGTACTCTGGGACCATGGAGTC 509

Db 575 ATCATCATGACCTGGAAAGTCTGCATCACTCTGGCTCC 634

Qy 510 CTTTATCCTGATTCTACCTGTGTTACCTTACCC

Db 635 CTCCCTGGCTATGGCTCATGTGAGCCTCATCCTAAAGACTGCCCTTGTGGCCTGTGAA 694

Qy 570 ATTATCACTTTTGTGAAATCTGGCTGTCTCAAACCTGGCTGTGAGATACC 627

Db 695 ATCAACAC-TTCTCTGTGAAACCTGTCAGCTGGCCTGTGATACC 751





/organism="Homo sapiens"  
/db\_xref="Taxon:9606"  
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/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1867  
High quality sequence stops: 304  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
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Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1867 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 304.  
Location/Qualifiers

modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the pET 7 and pET 7T vectors of the pET family.

vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. ".

Query Match 35.0%; Score 355; DB 9; Length 367;  
Best Local Similarity 100.0%; Pred. No. 3.9e-86;  
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Oy	231	TTCTTCCCTCACACCTGGCGTGCAGACATCGCTAACACGGTCCCCGG	290
Db	367	TTCTTCCCTCACACCTGGCGTGCAGACATCGCTAACACGGTCCCCGG	308
Oy	291	ATGCTGGTGAACCTCCTGCATCCAGCCAAAGCCATCTCCTTGGGGGGCATGATGCA	350
Db	307	ATGCTGGTGAACCTCCTGCATCCAGCCAAAGCCATCTCCTTGGGGGGCATGATGCA	248

QY	411	GATCTGTACGTGCCATCTGCCACCCCCCTCGATATTGCCATCATGACCTGGAGAGTC	470
Db	187	GATCTGTACGTGCCATCTGCCACCCCTCGATATTGCCATCATGACCTGGAGAGTC	128

Db 67 GTGTTACCTCTACCCCTCTGTAGGGCCAGAAATTATCACTTTTT 13

H62441  
LOCUS H62441  
DEFINITION yr79d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone  
IMAGE:211503 5' similar to SP:OLF7\_MOUSE P34984 OLFACTORY  
COMMENT: human ortholog of mouse olfactory receptor gene 7

ACCESSION RECEPTOR-LIKE PROTEIN K / ; mRNA sequence.  
VERSION H62441  
KEYWORDS H62441.1 GI:1015273  
SOURCE EST.  
human.

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1	(bases 1 to 426)

ADVISORS  
 Hillier, L., Lemond, G., Becker, M., Bonaldo, M.F., Chilabell, B.,  
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins  
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore  
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
 Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.  
 TITLE  
 Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)  
MEDLINE 97044478  
COMMENT Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

**BM670360**  
**LOCUS** BM670360  
**DEFINITION** UT-E-DWL-abc-b-11-0-UT-.s1  
**VERSION** 623 bp mRNA linear EST 27-FEB-2002  
**ORGANISM** HOMO sapiens cDNA clone

ACCESSION UI-E-DWL-ahc-b-11-0-01 3', mRNA sequence.  
 VERSION BM670360.1 GI:18980257  
 KEYWORDS EST.

SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 623)  
 AUTHORS Bonaldo, M.F.; Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9555  
 Email: msoares@blue.weeg.uiowa.edu

TISSUE Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics ([www.resgen.com](http://www.resgen.com)).

The following repetitive elements were found in this cDNA sequence: 95-137, >AT-rich#Low-complexity (matched compliment) 152-189, >(CAAA)n#Simple\_repeat (matched compliment)

Seq primer: M13 Forward

FEATURES Location/Qualifiers

source

1. .623  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-DWL"  
 /tissue\_type="lens"  
 /dev\_stage="adult"  
 /lab\_host="DHL0B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site\_1: Ecor I; Site\_2: Not I; UI-E-DWL is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the visual system, supported by National Eye Institute (NEI).  
 TAG\_LIB=UI-E-DWL  
 TAG\_SEQ=CGATTAGCGA"

BASE COUNT 148 a 159 c 107 g 209 t  
 ORIGIN

Query Match 34.1%; Score 345.6; DR 13; Length 623;  
 Best local Similarity 86.7%; Pred. No. 1.8e-83;  
 Matches 392; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 151 TTCTACGCTTCACCCCTGCTGGGAACGGGACATACTGGGCTCACTGGACTCC 210  
 DB 292 TTCTATGTCTCACCCCTGCTGGGAATGGGACATCCTCTGGGGCTCACTCACTGGACTCC 351  
 QY 211 AGACTGCACGCC-TGTACTTCTTCTCTCACACTGGGGCTGTCGACATGCCCTAC 269  
 DB 352 AGACTCACACCCCATGTACTTCTCTCACACTGGGGCTGTCACATGCCCTAC 411  
 QY 270 GCCTGCAACACGGTGGCCGGATGCTGGTGAACCTCTGCACTCCAGCCAGGCCATCTC 329  
 DB 412 GCCTGCAACACAGTGCCCCAGATGCTGGTGAACCTCTGCACTCCAGCCAAGGCCATCTC 471  
 QY 330 TTGGGGGGCGATGCGACCTTCTGTTCCACTTTCGTCAGAGAATGTC 389  
 DB 472 TTGCTGGCTGATGACATAGACCTTCTCTTGTAGTGCACATACTGAATGCTC 531  
 QY 390 CTCCCTGGGGTATGCTCATGACATGCTGAGCTGGCCACCTGGCATCCAGGCCAGGCCATCTC 591  
 DB 532 CTGTTGGTGTGAGTCCTACGATGGTACGGTACGGCCATCTGCCACCTCTCCGATATTTC 623  
 QY 450 GCCATCATGACCTGGAGAGTCTGCATCACCT 481  
 DB 592 ATCATCATGACCTGGAAAGTCGTCATCACCT 623

FEATURES Location/Qualifiers

source

1. .623  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-DWL"  
 /tissue\_type="lens"  
 /dev\_stage="adult"  
 /lab\_host="DHL0B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site\_1: Ecor I; Site\_2: Not I; UI-E-DWL is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the visual system, supported by National Eye Institute (NEI).  
 TAG\_LIB=UI-E-DWL  
 TAG\_SEQ=CGATTAGCGA"

BASE COUNT 148 a 159 c 107 g 209 t  
 ORIGIN

Query Match 34.1%; Score 345.6; DR 13; Length 623;  
 Best local Similarity 86.7%; Pred. No. 1.8e-83;  
 Matches 392; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 151 TTCTACGCTTCACCCCTGCTGGGAACGGGACATACTGGGCTCACTGGACTCC 210  
 DB 292 TTCTATGTCTCACCCCTGCTGGGAATGGGACATCCTCTGGGGCTCACTCACTGGACTCC 351  
 QY 211 AGACTGCACGCC-TGTACTTCTTCTCTCACACTGGGGCTGTCGACATGCCCTAC 269  
 DB 352 AGACTCACACCCCATGTACTTCTCTCACACTGGGGCTGTCACATGCCCTAC 411  
 QY 270 GCCTGCAACACGGTGGCCGGATGCTGGTGAACCTCTGCACTCCAGCCAGGCCATCTC 329  
 DB 412 GCCTGCAACACAGTGCCCCAGATGCTGGTGAACCTCTGCACTCCAGCCAAGGCCATCTC 471  
 QY 330 TTGGGGGGCGATGCGACCTTCTGTTCCACTTTCGTCAGAGAATGTC 389  
 DB 472 TTGCTGGCTGATGACATAGACCTTCTCTTGTAGTGCACATACTGAATGCTC 531  
 QY 390 CTCCCTGGGGTATGCTCATGACATGCTGAGCTGGCCACCTGGCATCCAGGCCAGGCCATCTC 591  
 DB 532 CTGTTGGTGTGAGTCCTACGATGGTACGGTACGGCCATCTGCCACCTCTCCGATATTTC 623  
 QY 450 GCCATCATGACCTGGAGAGTCTGCATCACCT 481  
 DB 592 ATCATCATGACCTGGAAAGTCGTCATCACCT 623

RESULT 15 A1285267/c

ACCESSION A1285267

LOCUS A1285267

DEFINITION q138c08.x1 NCI\_CGAP\_C08 Homo sapiens cDNA clone IMAGE:1874606 3', mRNA sequence.

KEYWORDS similar to SW:OLF7\_MOUSE P34984 OLFACTOY RECEPTOR-LIKE PROTEIN K7

SOURCE A1285267

VERSION A1285267.1 GI:3923500

COMMENT EST.

REFERENCE 1 (bases 1 to 361)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: [www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Insert Length: 659 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 26.

FEATURES Location/Qualifiers

source

1. .361  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1874606"  
 /clone\_lib="NCI\_CGAP\_C08"  
 /tissue\_type="adrenocarcinoma"  
 /lab\_host="DHL0B"  
 /note="Organ: colon; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT	115	a	73	c	110	g	63	t
ORIGIN								
Query Match	33.3%		Score	337.4		DB	9	
Best Local Similarity	96.9%		Pred. No.	2.5e-61		Length	361	
Matches	344		Conservative	0		Mismatches	11	
						Indels	0	
						Gaps	0	
Qy	231	TTCTTCCTCACACCTGGGGTCGGACATCGCCTACGGCTGCAACACGGTCCCCGG						
Db	361	TTTCCCTCACACCTGGGGTGGACATGCCTACGGCTGCAACACGGTCCCCGG						
Qy	291	ATGCTGGTGAACCTCCATCCAGGCAAGCCATCTCCTTGCGGGGGCATGAG						
Db	301	ATGCTGGTGAACCTCCATCCAGGCAAGCCATCTCCTTGCGGGGGCATGAG						
Qy	351	ACCTTCTGTTCCACTTGTGTCACAGATGTCCTCCTGGGGTATGCTAT						
Db	241	ACCTTCTGTTCCACTTGTGTCACAGATGTCCTCCTGGGGTAAAT						
Qy	411	GATCTGAGGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTC						
Db	181	GATTTGTACGTGGCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTC						
Qy	471	TGCATCACCTCGGGTACTCTGGACCTGGAGTCCTTATCTGTATCATCTT						
Db	121	TGCATCACCTCGGGTACTCTGGACCTGGAGTCCTTATCTGTATCATCTT						
Qy	531	GTGTTACTTACCTTACCTTCTGTAGGCCAGAAATTATCACTTTT						
Db	61	GTGTTACTTACCTTACCTTCTGTAGGCCAGAAATTATCACTTTT						

Search completed: May 2, 2003, 06:14:26  
 Job time : 1553 secs



GenCore version 5.1.4\_p5\_4578  
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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 04:33:51 ; Search time 2809 seconds  
(without alignments)  
10505.605 Million cell updates/sec

Title: US-09-898-586-23

Perfect score: 1014

Sequence: 1 taaacacttctcctaaccac.....tatggcattgtgactgacaa 1014

Scoring table: IDENTITY\_NUC

GapOp 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenEmbl:\*

2: gb\_ba:\*

3: gb\_htg:\*

4: gb\_in:\*

5: gb\_om:\*

6: gb\_ov:\*

7: gb\_pat:\*

8: gb\_ph:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pin:\*

35: em\_htg\_rnd:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htg\_o\_hum:\*

40: em\_htg\_o\_mus:\*

41: em\_htg\_o\_other:\*

## ALIGNMENTS

RESULT 1

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	
AX197458	AX197458	Sequence 23 from Patent WO0151632.	AX197458	AX197458.1	GI:15387838	human.	Homo sapiens	
							Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
							1 (bases 1 to 1014)	Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
							Spytek,K.A. and Li,L.	Odorant receptor polypeptides and nucleic acids encoding same

Pred. No. is the number of results predicted by chance to have a

JOURNAL	Patent: WO 0151632-A 23 19-JUL-2001;
FEATURES	Curagen Corporation (US)
source	Location/Qualifiers
1. .1014	
QY	/organism="Homo sapiens"
QY	/db_xref="taxon:9606"
BASE COUNT	218 a 281 c 216 g 299 t
ORIGIN	
Query Match	100.0%; Score 1014; DB 6; Length 1014;
Best Local Similarity	100.0%; Pred. No. 3.2e-239;
Matches	1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 TAAACACTCTCTAAACCATCACAGCTTAACTTGTGATTGGATATGGGG 60
QY	61 GACAATATAACATCCATCACAGAGTCTCTACTGGGATTCCGGTGGCCAAAGGATT 120
Db	61 GACAATATAACATCCATCACAGAGTCTCTACTGGGATTCCGGTGGCCAAAGGATT 120
QY	121 CAGATGCTCCCTTGGCTCTTCCCTGTTACGCTTCACCCGCTGGGAAACGGG 180
Db	121 CAGATGCTCCCTTGGCTCTTCCCTGTTACGCTTCACCCGCTGGGAAACGGG 180
QY	181 ACCATACTGGGGCTCATCTCACTGGACTCCAGTCACGCCCCCTGACTCTCCCT 240
Db	181 ACCATACTGGGGCTCATCTCACTGGACTCCAGTCACGCCCCCTGACTCTCCCT 240
QY	241 CACACCTGGGGTGTGGCCAGCATCGCTTACGGCTCCAGAGTGTGGTA 300
Db	241 CACACCTGGGGTGTGGCCAGCATCGCTTACGGCTCCAGAGTGTGGTA 300
QY	301 ACCCTCTGCAAGCCATCTCTTGGGGCCATGATGAGCTTCTGT 360
Db	301 ACCCTCTGCAAGCCATCTCTTGGGGCCATGATGAGCTTCTGT 360
QY	361 TTTCACCTTTGCTGTCAACAGATGTCTCTCTGGGGTGTATGATCTGTAG 420
Db	361 TTTCACCTTTGCTGTCAACAGATGTCTCTCTGGGGTGTATGATCTGTAG 420
QY	421 TGGCCATCTGCCACCCCCCTGGATATTGGCATCATGACCTGGAGAGCTCACCC 480
Db	421 TGGCCATCTGCCACCCCCCTGGATATTGGCATCATGACCTGGAGAGCTCACCC 480
QY	481 TCGGGGTGACTTCTGGGACACTGGAGCTTATCTTGATTCATCTGTGTTACTTC 540
Db	481 TCCGGGTGACTTCTGGGACACTGGAGCTTATCTTGATTCATCTGTGTTACTTC 540
QY	541 TACCTTACCCCTGTAGGCCAACATCAATGAGACATGGCTGGGGAGCA 600
Db	541 TACCTTACCCCTGTAGGCCAACATCAATGAGACATGGCTGGGGAGCA 600
QY	601 GTTCTCAAACCTGGCTGTGAGATACCTGAGATACCTGAGATGGCTGGCT 660
Db	601 GTTCTCAAACCTGGCTGTGAGATACCTGAGATACCTGAGATGGCTGGCTGGAGCA 660
QY	661 ATTCTCTGGGCTGGGGAGACCTGTGACATGAGAACATGGCTGGGGAGCA 720
Db	661 ATTCTCTGGGCTGGGGAGACCTGTGACATGAGAACATGGCTGGGGAGCA 720
QY	721 GCTATCCTCAGATCCAAAGGGAGTTGAGGAAGCTCTGACCTCTGCTCTCC 780
Db	721 GCTATCCTCAGATCCAAAGGGAGTTGAGGAAGCTCTGACCTCTGCTCTCC 780
QY	781 CACCTCTGTGATGGACTCTTATGGCACAGCCATATCATGATGTGGACCCAGA 840
Db	781 CACCTCTGTGATGGACTCTTATGGCACAGCCATATCATGATGTGGACCCAGA 840
QY	841 TATGGAAACCCCAAGGAGCAGAAGAATATCTCTGCTGTTACAGCTCTTATCCC 900
Db	841 TATGGAAACCCCAAGGAGCAGAAGAATATCTCTGCTGTTACAGCTCTTATCCC 900
QY	901 ATGCTCAATCCCTATCTGATGTTAGGAACTCAGAAGTGAAGAAACTTGAAGAGA 960
Db	901 ATGCTCAATCCCTATCTGATGTTAGGAACTCAGAAGTGAAGAAACTTGAAGAGA 960
QY	961 GTGCTGGAGTAGAAGGCTTATGAAAGGATATGGCATTTGACTGACAA 1014
Db	961 GTGCTGGAGTAGAAGGCTTATGAAAGGATATGGCATTTGACTGACAA 1014
RESULT 2	
AC004889/c	
REFERENCE	AC004889
LOCUS	130030 bp DNA linear
DEFINITION	PRI 14-JAN-1999
ACCESSION	Homo sapiens clone DJ0798C17, complete sequence.
VERSION	AC004889
KEYWORDS	AC004889.1 GI:4156187
SOURCE	HTG.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 130030)
TITLE	Waterston, R.H.
JOURNAL	The sequence of Homo sapiens clone
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 130030)
TITLE	Waterston, R.H.
JOURNAL	Direct Submission
REFERENCE	Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS	3 (bases 1 to 130030)
TITLE	Waterston, R.H.
JOURNAL	Direct Submission
REFERENCE	Submitted (14-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS	On Jan 14, 1999 this sequence version replaced g1:3213108.
COMMENT	Location/Qualifiers
FEATURES	1. .130030
source	/organism="Homo sapiens"
/clone="DJ0798C17"	
QY	/db_xref="taxon:9606"
BASE COUNT	38117 a 25410 c 26567 g 39936 t
ORIGIN	
Query Match	97.6%; Score 990; DB 9; Length 130030;
Best Local Similarity	99.8%; Pred. No. 3.4e-233;
Matches	1012; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Db	1 TAAACACTCTCTAACCATCACAGAGTCTCTACTGGGATTCCCGTGGCCAAAGGATT 60
QY	61 GACAATATAACATCCATCACAGAGTCTCTACTGGGATTCCCGTGGCCAAAGGATT 60
Db	61 GACAATATAACATCCATCACAGAGTCTCTACTGGGATTCCCGTGGCCAAAGGATT 60
QY	121 CAGATGCTCTTGGCTCTTCCCTACTGGGATTCCCGTGGCCAAAGGATT 180
Db	121 CAGATGCTCTTGGCTCTTCCCTACTGGGATTCCCGTGGCCAAAGGATT 180
QY	181 ACCATACTGGGGCTCATCTCACTGGACTCCAGACTGACGCCCTGCTGGGGAGCA 239
Db	181 ACCATACTGGGGCTCATCTCACTGGACTCCAGACTGACGCCCTGCTGGGGAGCA 239
QY	240 TCACACTCTGGGGTGTGAGCTACCTGCTGACCCATTCGCTGCTGGCTGGCTGG 299
Db	240 TCACACTCTGGGGTGTGAGCTACCTGCTGCTGGCTGGCTGGCTGGCTGG 299
QY	300 AACCTCTGCACTCCAGCCAGCCATCTCTCTTGGGGCCGATGATGCAAGGACCTTCTG 359
Db	300 AACCTCTGCACTCCAGCCAGCCATCTCTCTTGGGGCCGATGATGCAAGGACCTTCTG 359
QY	110997 AACCTCTGCACTCCAGCCAGCCATCTCTCTTGGGGCCGATGATGCAAGGACCTTCTG 110938

Query Match 97.4%; Score 987.4; DB 6; Length 1012;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-232;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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RESULT 3  
 AX197456  
 LOCUS AX197456 1012 bp DNA linear PAT 29-AUG-2001  
 DEFINITION Sequence 21 from patent WO0151632.  
 ACCESSION AX197456.1 GI:15387837  
 VERSION 1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1012)  
 AUTHORS Padigaru, M., Prayaga, S.K., Taupier, R.J., Mishra, V., Tchernev, V.T.,  
 Spytek, K.A. and Li, L.  
 TITLE Odorant receptor polypeptides and nucleic acids encoding same  
 JOURNAL Patent: WO 0151632-A 21 19-JUL-2001;  
 Curagen Corporation (US)  
 FEATURES source  
 /organism="Homo sapiens"  
 1. .1012  
 BASE COUNT 219 a 281 c 215 g 297 t  
 ORIGIN

Query Match 97.4%; Score 987.4; DB 6; Length 1012;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-232;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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RESULT 4  
 AX197438  
 LOCUS AX197438 1040 bp DNA linear PAT 29-AUG-2001  
 DEFINITION Sequence 3 from patent WO0151632.







Db 21953 TGTCTCAAATTCGCTGTGCAGATCCCACATCAATGAGAACATGGCTGGCCGGAGC 21894  
 QY 660 ATTCTGGCTGGGACCCTTGTCACAAATTGTTCATATGTGCATCCCTCTG 719  
 Db 21893 AATTCTGGCTGGCACCTTGTCACATGTAGTTCATATGTGCATCCCTCTG 21834  
 QY 720 TCTATCCTCAGATCCAATCAAGGAAGTCAGAGGAAGCCATTGACCTGCTTC 779  
 Db 21833 TCTATCCTCAGATCCAATCAAGGAAGTCAGAGGAAGCCTTCGCACCTGCTTC 21774  
 QY 780 CCACCTCTGCTGACTCTTATGGCACAGCCATTATGCACAGCCATTATCATGTATGTTGACCCAG 839  
 Db 21773 ATATGGGAACCCCAAGGAGCAGAAGAAATATCTCCTGCTGTTTCACAGCCTCTTAATCC 899  
 QY 900 CATGCTCAATCCCTTATCTGTAGCTTAGAACTCAGAAGTGAAGAACTTGTGAAGAG 959  
 Db 21653 CATGCTCAAATCCCCTATCTGTAGCTTAGAACTCAGAAGTGAAGAACTTGTGAAGAG 21594  
 QY 960 AGTGCTGGGAGTAGAAAGGCTTTATGAAAGGATTATGGCATGTGACTGACA 1013  
 Db 21593 AGTGCTGGGAGTAGAAAGGCTTTATGAAAGGATTATGGCATGTGACTGACA 21540

RESULT 7

AC005587	AC005587	140915	bp	DNA	linear	PRI	21-DEC-11
LOCUS	DEFINITION	Homo sapiens PAC clone RP5-988G15 from 7q33-q35, complete sequence					
ACCESSION	ACCESSION	AC005587					
VERSION	VERSION	AC005587.1 GI:4156166					
KEYWORDS	KEYWORDS	HTG.					
SOURCE	SOURCE	Homo sapiens.					
ORGANISM	ORGANISM	Homo sapiens					
REFERENCE	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi					
AUTHORS	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	TITLE	1 (bases 1 to 140915)					
JOURNAL	JOURNAL	Hou, S., Wohldmann, P. and Le, T.					
REFERENCE	REFERENCE	The sequence of <i>Homo sapiens</i> PAC clone RP5-988G15					
AUTHORS	AUTHORS	Unpublished					
TITLE	TITLE	2 (bases 1 to 140915)					
JOURNAL	JOURNAL	Waterston, R.H.					
REFERENCE	REFERENCE	Direct Submission					
AUTHORS	AUTHORS	Submitted (01-SEP-1998) Genome Sequencing Center, Washington					
TITLE	TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis					
JOURNAL	JOURNAL	MO 63108, USA					
REFERENCE	REFERENCE	3 (bases 1 to 140915)					
AUTHORS	AUTHORS	Waterston, R.H.					
TITLE	TITLE	Direct Submission					
JOURNAL	JOURNAL	Submitted (14-JAN-1999) Genome Sequencing Center, Washington					
REFERENCE	REFERENCE	University School of Medicine, 4444 Forest Park Parkway, St. Louis					
AUTHORS	AUTHORS	MO 63108, USA					
TITLE	TITLE	4 (bases 1 to 140915)					
JOURNAL	JOURNAL	Waterston, R.					
REFERENCE	REFERENCE	Direct Submission					
AUTHORS	AUTHORS	Submitted (15-JAN-1999) Department of Genetics, Washington					
TITLE	TITLE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,					
JOURNAL	JOURNAL	5 (bases 1 to 140915)					
REFERENCE	REFERENCE	Waterston, R.					
AUTHORS	AUTHORS	Direct Submission					
TITLE	TITLE	Submitted (21-DEC-1999) Department of Genetics, Washington					
JOURNAL	JOURNAL	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,					
COMMENT	COMMENT	On Jan 14, 1999 this sequence version replaced gi:3907499.					
----- Genome Center							
Center: Washington University Genome Sequencing Center							
Center code: WUGSC							
Web site: <a href="http://genome.wustl.edu/gsc">http://genome.wustl.edu/gsc</a>							
Contact: <a href="mailto:sapiens@watson.wustl.edu">sapiens@watson.wustl.edu</a>							
----- Summary Statistics							
Center project name: H_DJ0988G15							

**NOTICE:** This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

**MAPPING INFORMATION:**

The sequence of this clone was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**SOURCE INFORMATION:**

This clone was derived from human PAC Library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., *Nature Genetics* 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

**VECTOR:** pcYPAC2

**NEIGHBORING SEQUENCE INFORMATION:**

Actual start of this clone is at base position 1 of RP5-988G15. Actual end is at 140915 of RP5-988G15.

**FEATURES**

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Best Local Similarity 99.4%; Pred. No. 1.3e-231; Mismatches 4; Indels 2; Gaps 2;
Matches 1008; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db 101725 ACCATACTGGGGCTCATCTCACTGGACTCCAGACTGCTGACACGGGCCCCATGCTGGG 101784
QY 240 TCACACCTGGGGCTGCTGACATCGGCTTACGGCTGCAACACGGGCCCCATGCTGGG 299
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RESULT 8  
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LOCUS AX078373  
DEFINITION Sequence 41 from Patent WO0107612.  
ACCESSION 974 bp DNA linear PAT 22-FEB-2001  
VERSION AX078373.1 GI:13158042  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 974)  
AUTHORS Au-Young, J., Bandman, O., Tang, Y.T., Yue, H., Aztmzai, Y., Burford, N., Baughn, M.R., Lu, D.A., Hillman, J.L., Patterson, C. and Lal, P.  
TITLE Receptors and associated proteins  
JOURNAL Patent: WO 0107612-A 41 01-FEB-2001;  
FEATURES source  
1. .974  
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BASE COUNT 206 a 270 c 214 g 284 t  
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Matches 958; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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LOCUS AX242191  
DEFINITION Sequence 939 from Patent WO0127158.  
ACCESSION AX242191.1 GI:15799066  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 930)  
AUTHORS Bellinson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.  
TITLE Olfactory receptor sequences  
JOURNAL Patent: WO 0127158-A 939 19-APR-2001;  
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 VERSION AX451262.1 GI:21698331  
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 SOURCE unidentified.  
 ORGANISM unclassified.  
 REFERENCE 1.  
 AUTHORS Hubert, R.S., Raitano, A.B., Faris, M., Challita-Eid, P.M., Ge, W. and Jakobovits, A.  
 TITLE Nucleic acids and corresponding proteins entitled phorl-all and Phorl-f5d6 useful in treatment and detection of cancer  
 JOURNAL Patent: WO 0214501-A 1455 21-FEB-2002; Agensys, Inc. (US)  
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Query Match 89.1%; Score 903.6; DB 6; Length 933;  
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ACCESSION	AX241442		
VERSION	AX241442.1		
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SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 930)		
TITLE	Bellenson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.		
JOURNAL	Olfactory receptor sequences		
FEATURES	Patent: WO 0127158-A 190 19-APR-2001;		
SOURCE	Digiscents (US); YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)		
BASE COUNT	193 a 265 c 202 g 270 t		
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Qy	294	CTGGTGAACCTCTGCATCCAGCCAAGGCCATCTCCTTGGGGCGATGCGACCC	353
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Qy	414	CTGGTACGGCATCTGCCACCCCTCGATATTGGCCATCATGACCCGGAGACTGC	473
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Qy	474	ATCACCCCTGGGGTGAACCTCTGGACCACTGGAGCTCTTTATCCTGATTCACTTGTG	533
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Qy	774	CTTCTCCCACCTCTGTTGACTCTTCAGATCCAAAGGAAGTCAGAGGAAGCCTTCCGACCTG	833
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Db	780	ACCCAGATATGGAAACCCCAAGGAGCAGAAGAAATATCCTGCTGTTCACAGCCTCTT	839
Qy	894	TAATCCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACCTAGAAGTAACCTT	953
Db	840	TAATCCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACCTAGAAGTAACCTT	899
Qy	954	GAAGAGAGTCTGGGAGTAGAAAGGCTTA	984
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RESULT	12		
AX241473			
LOCUS	AX241473	930 bp	DNA
DEFINITION	Sequence 221 from Patent WO0127158.		
ACCESSION	AX241473		
VERSION	AX241473.1		
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 930)		
TITLE	Bellenson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.		
JOURNAL	Olfactory receptor sequences		
FEATURES	Patent: WO 0127158-A 221 19-APR-2001;		
SOURCE	Digiscents (US); YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)		
BASE COUNT	193 a 265 c 202 g 270 t		
ORIGIN			
Query Match	88.8%	score 900.6; DB 6; Length 930;	
Best Local Similarity	99.4%	Pred. No. 2.9e-211;	
Matches	925; Conservative	0; Mismatches 4; Indels 2; Gaps 2;	
Qy	55	ATGGGGACAAATACATCCATCACAGAGTCTCTACTGGATTCCCGTTGGCCA	114
Db	1	ATGGGAGACAAATACATCCATCACAGAGTCTCTACTGGATTCCCGTTGGCCA	60
Qy	115	AGGATTCAAGATGCTCTTGGCTCTCCCTACTGGATTCCCGTTCTACGGTCTCACCCCTGGGG	174
Db	61	AGGATTCAAGATGCTCTTGGCTCTCCCTACTGGATTCCCGTTCTACGGTCTCACCCCTGGGG	120
Qy	175	AACGGGACCATACTGGGGTCACTCACTGGACTCCAGACTGCACGCCCTGGCTGGGG	233
Db	121	AACGGGACCATACTGGGGTCACTCACTGGACTCCAGACTGCACGCCCTGGCTGGGG	180
Qy	234	TTCTCTCACACCTGGGGTGGACATCGCCTACGGCTGGCAACACGGTCCCCGGAT	293

		REFERENCE	3 (bases 1 to 104955)
Db	181	AUTHORS	Waterson, R.H.
QY	294	TITLE	Direct Submission
Db	241	DEFINITION	Submitted (31-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
QY	354	ACCESSION	4 (bases 1 to 104955)
Db	301	VERSION	Submitted (31-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
QY	414	KEYWORDS	5 (bases 1 to 104955)
Db	361	ORGANISM	Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
QY	474	FEATURES	5 (bases 1 to 104955)
Db	421	SOURCE	Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
QY	534	REFERENCE	On Aug 9, 2001 this sequence version replaced gi:14550325.
Db	481	AUTHORS	Waterson, R.
QY	594	TITLE	Direct Submission
Db	540	COMMENT	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
QY	654	JOURNAL	Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Db	600	REFERENCE	On Aug 9, 2001 this sequence version replaced gi:14550325.
QY	714	AUTHORS	Waterson, R.
Db	660	TITLE	Direct Submission
QY	774	DEFINITION	Center: Washington University Genome Sequencing Center
Db	720	ACCESSION	Center code: WUGSC
QY	834	VERSION	Web site: <a href="http://genome.wustl.edu/gsc">http://genome.wustl.edu/gsc</a>
Db	780	KEYWORDS	Contact: <a href="mailto:sapiens@watson.wustl.edu">sapiens@watson.wustl.edu</a>
QY	894	FEATURES	-----
Db	840	SOURCE	-----
QY	954	REFERENCE	-----
Db	900	AUTHORS	-----
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.			
This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.			
MAPPING INFORMATION: The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <a href="http://www.nhgri.nih.gov/DIR/GTB/CHR7">http://www.nhgri.nih.gov/DIR/GTB/CHR7</a> , send mailto: <a href="mailto:egreen@nhgri.nih.gov">egreen@nhgri.nih.gov</a> , or see <a href="http://genome.wustl.edu/gsc">http://genome.wustl.edu/gsc</a>			
SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. ( <a href="http://www.resgen.com">http://www.resgen.com</a> ) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute ( <a href="http://bacpac.med.buffalo.edu">http://bacpac.med.buffalo.edu</a> )			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 104955)	FEATURES	1. .104955
AUTHORS	Sulston, J.E. and Waterston, R.	SOURCE	/organism="Homo sapiens"
TITLE	Toward a complete human genome sequence	VECTOR	/db_xref="taxon:9606"
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)	NEIGHBORING SEQUENCE INFORMATION:	/chromosome="7"
MEDLINE	99063792	The clone sequenced to the left is RP4-669B10, 2000 bp overlap; the clone sequenced to the right is RP4-798C17, 2000 bp overlap.	
PUBLMED	9847074	Actual start of this clone is at base position 123947 of RP4-669B10; actual end is at base position 64342 of RP11-798C17.	
REFERENCE	2 (bases 1 to 104955)	RP11-703N5 contains a single plasmid region from 4530 to 4616 and 4668 to 4721.	
AUTHORS	Harris, A., Haakenson, W. and Spalding, L.	LOCATION/QUALIFIERS	
JOURNAL	The sequence of Homo sapiens BAC clone RP11-703N5	LOCATION	
	Unpublished (2001)	QUALIFIERS	



Db 29255 GCCCTTGTCACTCTAGTGTACTGCTTACACTGCTCTGGACCCAGAACTTA 29314 \* the accession number will be preserved.  
 QY 575 TCACTTTTGTGAATCTGGCTCTCAACTGCTGTGAGATAACCCACATCA 634 \* 1 1127: contig of 11127 bp in length  
 Db 29315 TCAC-TTTTCTGTGAATTATGGCTGCTCTCAACTGCTGTGAGATAACCCACATCA 29373 \* 11128 11227: gap of unknown length  
 QY 635 ATGAGAACATGGCTGGCGGAGCAATTCTGGCTGGGGACCCCTGTCCACATTG 694 \* 11228 18868: gap of unknown length  
 Db 29374 ATGAGGTATGGTTTGCGAGGGCAGTGTCTGTGCTGGGGAGCCCTTCCACTG 29433 \* 18969 40960: contig of 21992 bp in length  
 QY 695 TAGTTCATATATGTGCATCCCTCTGCTCTCCACCTCTGTGTGGACTCTTTATGGCACAG 754 \* 40961 41060: gap of unknown length  
 Db 29434 TATATATCTTATGTTCATATTCTATGTGCCCCAGTCACTTAAGATTCAGGAGGGGTGCC 29493 \* 41061 44591: contig of 3531 bp in length  
 QY 815 CCATTATCACTGATGGACCCAGATAGGAAACCCAGGAGCAGAAATACCTCC 874 \* 44592 44691: gap of unknown length  
 Db 29554 CCATCATCATGTATGTGAGGCCAGTATGAGGCCAGGAGCAGAAATACCTCC 29613 \* 44692 46067: contig of 1375 bp in length  
 QY 875 TGCCTGTTCACAGCCTCTTAATCCATGCTCAATCCCTATCTGTAGCTTAGGACT 934 \* 46068 46167: gap of unknown length  
 Db 29614 TGCTGTTCACAGCCTCTCAATCCCATGCTTAATCCCTAATTATAGCTTAGGACA 29673 \* 46168 47511: contig of 1344 bp in length  
 QY 935 CAGAAGTGAAGAATACTTGAAGAGACTGCTGGAGTAGAAAGGGCTTATGAAA 989 \* 47512 47611: gap of unknown length  
 Db 29674 AGGAAGTCCAAAGGTACTCTAAAGAGATGCTGAAGAGAACTTCATGAAA 29728 \* 47612 51354: contig of 3743 bp in length  
 RESULT 14 \* 51355 51454: gap of unknown length  
 AC091746 \* 51455 52639: contig of 1185 bp in length  
 LOCUS AC091746 204316 bp DNA linear HTG 26-APR-2002 \* 52640 52739: gap of unknown length  
 DEFINITION MUS musculus chromosome 6 clone RP23-62E15 map 6B2, \*\*\* SEQUENCING \* 52740 54199: contig of 1460 bp in length  
 ACCESSION AC091746 \* 54200 54299: gap of unknown length  
 VERSION AC091746.2 GI:20331040 \* 54299 70626: gap of unknown length  
 KEYWORD HTG; HTGS\_PHASE2. \* 70626 74065: contig of 8894 bp in length  
 SOURCE Mus musculus. \* 74066 74166: 77890: contig of 3725 bp in length  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; \* 77891 77990: gap of unknown length  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. \* 77991 82776: contig of 4786 bp in length  
 REFERENCE 1 (bases 1 to 204316) \* 82776 82876: gap of unknown length  
 AUTHORS Young, J.M., Madan, A., Hall, J., Friedman, C., Dickhoff, R., Greene, J., \* 82877 90955: contig of 8079 bp in length  
 TITLE Evolution of the mouse olfactory receptor gene family \* 90956 91055: gap of unknown length  
 JOURNAL Submitted (28-MAY-2001) Division of Human Biology, Fred Hutchinson \* 91056 93563: contig of 2508 bp in length  
 REFERENCE 2 (bases 1 to 204316) \* 93563 93663: gap of unknown length  
 AUTHORS Young, J.M., Madan, A., Hall, J., Friedman, C., Dickhoff, R., Greene, J., \* 93663 93564: gap of 4876 bp in length  
 TITLE Direct Submission \* 93564 98540: gap of unknown length  
 JOURNAL Submitted (28-MAY-2001) Division of Human Biology, Fred Hutchinson \* 98540 100233: contig of 1594 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 100233: gap of unknown length  
 AUTHORS Lane, R.P. and Trask, B.J. \* 100334: 108744: contig of 8411 bp in length  
 TITLE Unpublished \* 108744: gap of unknown length  
 JOURNAL Cancer Research Center, 1100 Fairview Ave N, C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA \* 108844: gap of 11740 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 108844: contig of 11740 bp in length  
 AUTHORS Young, J.M., Madan, A., Hall, J., Friedman, C., Dickhoff, R., Greene, J., \* 120584: gap of unknown length  
 TITLE Direct Submission \* 120584: contig of 1550 bp in length  
 JOURNAL Submitted (26-APR-2002) Division of Human Biology, Fred Hutchinson \* 120585 122334: contig of 1550 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 122334: gap of unknown length  
 AUTHORS Rodrigues, S., Kettnerman, M., Fahey, J., Helton, E., Sanchez, A., \* 122335 136966: contig of 14632 bp in length  
 Madan, A., Whiting, M., Ross, J.A., Lane, R.P. and Trask, B.J. \* 136966 136967: gap of unknown length  
 TITLE Direct Submission \* 136967 137066: gap of unknown length  
 JOURNAL Cancer Research Center, 1100 Fairview Ave N, C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA \* 137067 146815: contig of 9749 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 146815 146916: gap of unknown length  
 AUTHORS Young, J.M., Madan, A., Hall, J., Friedman, C., Dickhoff, R., Greene, J., \* 146916 152543: contig of 5628 bp in length  
 TITLE Direct Submission \* 152543 152643: gap of unknown length  
 JOURNAL Submitted (28-MAY-2001) Division of Human Biology, Fred Hutchinson \* 152643 164250: contig of 11607 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 164250 164350: gap of unknown length  
 AUTHORS Lane, R.P. and Trask, B.J. \* 164350 170223: contig of 5873 bp in length  
 TITLE Direct Submission \* 170223 170323: gap of unknown length  
 JOURNAL Submitted (26-APR-2002) Division of Human Biology, Fred Hutchinson \* 170323 189235: contig of 18912 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 189235 189335: gap of unknown length  
 AUTHORS Rodriguez, S., Kettnerman, M., Fahey, J., Helton, E., Sanchez, A., \* 189335 189336: gap of unknown length  
 Madan, A., Whiting, M., Ross, J.A., Lane, R.P. and Trask, B.J. \* 189336 199422: contig of 10087 bp in length  
 TITLE Direct Submission \* 199422 199522: gap of unknown length  
 JOURNAL Submitted (26-APR-2002) Division of Human Biology, Fred Hutchinson \* 199522 201282: contig of 1760 bp in length  
 REFERENCE 3 (bases 1 to 204316) \* 201282 201382: gap of unknown length  
 AUTHORS Rodriguez, S., Kettnerman, M., Fahey, J., Helton, E., Sanchez, A., \* 201382 204316: contig of 2934 bp in length.  
 TITLE Direct Submission \* 204316  
 JOURNAL Cancer Research Center, 1100 Fairview Ave N, C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA  
 COMMENT On Apr 26, 2002 this sequence version replaced gi:14211553. \* 1. .204316  
 \* NOTE: This is a 'working draft' sequence. It currently \* /organism="Mus musculus"  
 \* consists of 30 contigs. Gaps between the contigs \* /db\_xref="taxon:10090"  
 \* are represented as runs of N. The order of the pieces \* /chromosome="6"  
 \* is believed to be correct as given, however the sizes \* /map="6B2"  
 \* of the gaps between them are based on estimates that have \* /clone="RP23-62E15"  
 \* provided by the submittor. \* 1. .204316  
 \* This sequence will be replaced \* 1. .204316  
 \* by the finished sequence as soon as it is available and \* 1. .204316

FEATURES source  
 BASE COUNT 61234 a 39664 c 38680 g 61651 t 3087 others  
 ORIGIN  
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 Best Local Similarity 80.5%; Pred. No. 3.2e-148;  
 Matches 779; Conservative 0; Mismatches 187; Indels 2; Gaps 2;

QY	25	CATTAACCTGATTCCCTCTGTCAAGGATATGGGGACAAATAACATCCATCACAGAG	84	DEFINITION	Homo sapiens clone OR2A7 olfactory receptor gene, partial cds.
Db	117956	CATGAATTTCAGTTCCCTCTGTCAAGGATATGGGAACAAATAGACATAACAGAG	118015	ACCESSION	AF399598
QY	85	TCCCTCTACTAGTGGATTCGGGTTGGCCAAAGGATTCAGATGCTCTCTGGCTCTTC	144	VERSION	AF399598.1 GI:15293780
Db	118016	TTCATCTCTCTGNGATTCCTCTCACGGATATGGAAACAAATAGACATAACAGAG	118075	KEYWORDS	.
QY	145	TCCCTCTACTAGTGGATTCGGGTTGGCCAAAGGATTCAGATGCTCTCTGGCTCTTC	204	SOURCE	Homo sapiens.
Db	118076	TCCCTCTCTTATGCCTTCACCGCTGCTGGGAATGGAAACCAATCTGACATCGACAG	118135	ORGANISM	Homo sapiens
QY	205	GACTCCAGACTGCACGC-CCACTGACTCTCTCACACCTGGGGTGTGACATC	263	REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Db	118136	GACTCCAGACTCCACACTCCATGACTCTCTCTCATCTGGCATCGTGTGACATT	118195	AUTHORS	1 (bases 1 to 650)
QY	264	GCCTACGCCGCAACACGGTGGCCCGATGCTGGTGAACCTCCCTGCATCCAGCCC	323	TITLE	Fuchs,T., Malecova,B., Linhart,C., Sharan,R., Khen,M., Herwig,R., Shmulevich,D., Elkon,R., Steinbach,M., O'Brien,J.K., Radelof,U., Lehrach,H., Olender,Z., Gluesman,G., Lancet,D. and Shamir,R.
Db	118196	GCCTATGCCGCAACACAGTGGCCAGATGGTGAACCTTTAGATCCAGTGAAGCC	118255	REFERENCE	DEROG: A Practical Scheme for Deciphering Families of Genes
QY	324	ATCTCCTTGCGGCCATGATGAGCTGAGACTTCTGTTCCACTTTGCTGTCAGAGA	383	AUTHORS	Unpublished
Db	118256	ATTCTCTAGCTGGTGTATGACACAGACTTTCTCTTGTGACATTGCTATCCACAGAA	118315	TITLE	2 (bases 1 to 650)
QY	384	TGTCTCTCTGGTGTATGTCATCTGTACGTGCCATCTGCCACCCCTCCGA	443	JOURNAL	Fuchs,T., Malecova,B., Linhart,C., Sharan,R., Khen,M., Herwig,R., Shmulevich,D., Elkon,R., Steinbach,M., O'Brien,J.K., Radelof,U., Lehrach,H., Olender,Z., Gluesman,G., Lancet,D. and Shamir,R.
Db	118316	TGCCTCTCTAGTGGTGTATGTCATCTGTACCTCCATGACCGGTATGTGCAATCTGTCAACCACTCCGT	118375	REFERENCE	Submitted (16-JUL-2001) Dept. of Molecular Genetics and the Crown
QY	444	TATTTGGCCATCATGACCTGGAGAGTCTGCATCACCTGTTACTCTACCTTACCCCTGTAGGCC	503	AUTHORS	Human Genome Center, Weizmann Institute of Science, Rehovot 76100, Israel
Db	118376	TACTCTGCCATCATGACCTGGAGAGTGTGCACTTACCCCTGTGTGATT	118435	TITLE	1. .>650
QY	504	GAGAGCTTTATCCTGATCATCTGTTACTCTACCTTACCCCTGTAGGCC	563	JOURNAL	Location/Qualifiers
Db	118436	GTTGTTCTGCTGCTTGTATCCACCTCGTGTACTTTACCCCTGTGTGTCT	118495	FEATURES	1. .>650
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Db	118496	CAGAAAGTGTACACAC-TTTTCTGTGAATTACAGCTATCTCAACACTTGCTGTGCAAGA	118554	mrRNA	/db_xref="taxon:9606"
QY	624	TACCCACATCAATGAGAACATGGCTGGGGAGCAATTCTGGGCTGGGGACCCCT	683	CDS	/chromosome="7"
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QY	684	GTCCACAATGTAGTTCATATATGTCATCTCTGTGCTATCTTCAGATCAAAG	743	SOURCE	/clone="OR2A7"
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QY	744	GGAAGTCAAGGAAAGCCTCTCACCTGCTCTGTGCTATCTTCAGATCAAAG	803	CDS	/note="contains transmembrane regions 2-7"
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QY	864	GAATATCTCTGTTCACACCTCTTAACTCCATGCTCAATCCCTATCTGTAG	923	CDS	/db_xref="GI:15293781"
Db	118795	GAATATCTCTGCTTCAAGCTTAAACCTATGCTCAACCCCTGATCTAG	118854	FEATURES	/translation="VVDIAYACNTVPRMLVNLLHPAKPISAGRMOMFLFSTFADVTE
QY	924	TCTTAGGAACCTCAGAAGAAACTTGAAGAGAGTCTGGGAGTAGAACGGCTT	983	SOURCE	CLIVVMSDLYVAICHPLRYLAIMTWRCVITLAVTSWTTGVLSSLLHVLVLLPLFC
Db	118855	TCTCAGGAATCTGACGTGAAGAATACATGAAAGAGTCTGGAGACACAGAGCTT	118914	mrRNA	RPQKTYHFFCEILAVLKLACADTHINENMVLAGAISGLVGPLSTIVSYMCILCAIQ
QY	984	ATGAAAG 991		BASE COUNT	LOSREYRORKAECTCFSHLCVIGLYFYTAIIMYVGPRYGNPKEOKKYLPLFHSLENP.
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Best Local Similarity					
Matches 649; Conservative					
Score 637 4; DB 9; Length 650;					
Pred. No. 2.3e-146; Mismatches 0; Indels 1; Gaps 1;					
Matches 649; Conservative					
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Matches 649; Conservative					
Score 637 4; DB 9; Length 650;					
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Score 637 4; DB 9; Length 650;					
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Matches 649; Conservative					
Score 637 4; DB 9; Length 650;					
Pred. No. 2.3e-146; Mismatches 0; Indels 1; Gaps 1;					
Matches 649; Conservative					
Score 637 4; DB 9; Length 650;					
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Score 637 4; DB 9; Length 650;					
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Qy	732	GATCCAATCAAGGGAAGTTCAGAGGAAGCCTCTGCACCTGCTCTCCCACCTCTGTG	791
Db	480	GATCCAATCAAGGGAAGTTCAGAGGAAGCCTCTGCACCTGCTCTCCCACCTCTGTG	539
Qy	792	GATGGACTCTTATGGCACAGCCATTATCATGTATGTTGGACCCAGATATGGAACCC	851
Db	540	GATGGACTCTTATGGCACAGCCATTATCATGTATGTTGGACCCAGATATGGAACCC	599
Qy	852	CAAGGACGAGAAATATCTCCTGCTGTTCACAGCCTTTAATCCCAT	902
Db	600	CAAGGAGCAGAAGAATATCTCCCGCTGTTCACAGCCTTTAATCCCAT	650

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Job time : 3242 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 04:56:35 ; Search time 1671 Seconds  
 (without alignments)  
 717.034 Million cell updates/sec

Title: US-09-898-586-23

Perfect score: 1014

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

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10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1

; Sequence 23, Application US/09898586

; Publication No. US20030077794A1

; GENERAL INFORMATION:

; APPLICANT: Gerlach, Valerie L

; APPLICANT: Macdougall, John R

; APPLICANT: Smithson, Glenna

; TITLE OF INVENTION: No. US20030077794A1

; FILE REFERENCE: 15966-638C1P

; CURRENT APPLICATION NUMBER: US/09/898,586

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: 09/761,288

; PRIOR FILING DATE: 2001-01-16

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 100.0%; Score 1014; DB 9; Length 1014;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 111, APP

Sequence 22, APP

Sequence 135, APP

Sequence 228, APP

Sequence 326, APP

Sequence 10, APP

Sequence 176, APP

Sequence 5098, APP

Sequence 21, APP

Sequence 15, APP

Sequence 290, APP

Sequence 378, APP

Sequence 70, APP

Sequence 254, APP

Sequence 470, APP

Sequence 66, APP

Sequence 1, APP

Sequence 3, APP

Sequence 7, APP

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 ; Sequence 23, Application US/09761288  
 ; Patent No. US20020065405A1

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 RESULT 3  
 US-09-898-586-21  
 Sequence 21, Application US/09898586  
 Publication No. US20030077794A1  
 GENERAL INFORMATION:  
 APPLICANT: Gerlach, Valerie L  
 APPLICANT: MacDougall, John R  
 APPLICANT: Smithson, Glenna  
 TITLE OF INVENTION: No. US20030077794A1 Polypeptides and Nucleic Acids Encoding Same  
 FILE REFERENCE: 15966-638C1P  
 CURRENT APPLICATION NUMBER: US/09/898, 586  
 CURRENT FILING DATE: 2001-08-27  
 PRIORITY NUMBER: 60/177, 839  
 PRIORITY FILING DATE: 2000-01-25  
 PRIORITY NUMBER: 60/176, 134  
 PRIORITY FILING DATE: 2000-01-14  
 PRIORITY NUMBER: 60/175, 989  
 PRIORITY FILING DATE: 2000-01-13  
 PRIORITY NUMBER: 60/218, 324  
 PRIORITY FILING DATE: 2000-07-14  
 PRIORITY NUMBER: 60/220, 253  
 PRIORITY FILING DATE: 2000-07-24  
 PRIORITY NUMBER: 60/178, 191  
 PRIORITY FILING DATE: 2000-01-26  
 PRIORITY NUMBER: 60/178, 227  
 PRIORITY FILING DATE: 2000-01-26  
 PRIORITY NUMBER: 60/220, 590  
 PRIORITY FILING DATE: 2000-07-25  
 PRIORITY NUMBER: 09/761, 288  
 PRIORITY FILING DATE: 2001-01-16  
 NUMBER OF SEQ ID NOS: 104  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 21  
 LENGTH: 1012  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 Query Match 97.4%; Score 987.4; DB 9; Length 1012;  
 Best Local Similarity 99.7%; Pred. No. 5.2e-312;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 2; Gaps 0;  
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 Qy 62 ACAATATAACATCCATCACAGAGTTCCCTACTGGATTCCCGTTGGCCAAGGATC 121  
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 Qy 182 CCATACTGGGCTCATCTCACTGGACTCCAGCTCACGCCACGGCCCC-TGTACTCTTCCTC 240  
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 Qy 241 CACACCTGGGGTGTGACATGGCTACGGCTTACGGCTTACGGCTTTAATCCC 300  
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 Qy 361 TTCCACTTTGCTCACAGAATGTCTTGGCATATGACCTGGAGAGTCTGCATCACCC 420  
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 Qy 421 TGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGCATCACCC 480  
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 Qy 781 CACCTCTGTTGATGGACTCTTATGCCACAGCCATTATCATGATGTTGGACCCAGA 840  
 Db 780 CACCTCTGTTGATGGACTCTTATGCCACAGCCATTATCATGATGTTGGACCCAGA 839  
 Qy 841 TATGGAAACCCCAAGGAGCAGAGAAATATCTCCTGCTGTTCACGCCCTTAAATCCC 900  
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 Qy 901 ATGCTCAAATCCCCTATCTGTTAGGAACTCAGAAGTCTGCACCTCTGC 960  
 Db 900 ATGCTCAAATCCCCTATCTGTTAGGAACTCAGAAGTCTGCACCTCTGC 959  
 Qy 961 GTGCTGGGAGTAGAAAGGCTTATGAAAGGATTATGCCATTTGTGACTGACAA 1013  
 Db 960 GTGCTGGGAGTAGAAAGGCTTATGAAAGGATTATGCCATTTGTGACTGACAA 1012

RESULT 4

US-09-761-288-21

; Sequence 21, Application US/09761288

; Patent No. US20020065405A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberky

; APPLICANT: Li, Li

TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding San FILE REFERENCE: 15966-638

CURRENT APPLICATION NUMBER: US/09/761, 288

CURRENT FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 60/177, 839

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 60/176, 134

PRIOR FILING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: 60/175, 989

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: 60/218, 324

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/220, 253

PRIOR FILING DATE: 2000-07-24

PRIOR APPLICATION NUMBER: 60/178, 191

PRIOR FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/178, 227

PRIOR FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/220, 590

PRIOR FILING DATE: 2000-07-25

NUMBER OF SEQ ID NOS: 95

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 1012

TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-761-288-21

Query Match 97.4%; Score 987.4; DB 10; Length 1012;

Best Local Similarity 99.7%; Pred. No: 5.2e-312;

Matches 1010; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 2 AACACTCTCTAAACCATGAGCATACTTGTGTCATAGGATATGGGG 61

Db 1 AACACTCTCTAAACCATGAGCATACTTGTGTCATAGGATATGGGG 60

Db 61 ACAATAAACATCCACAGAGTCTCTACTGGGATTCCGGCCAAAGGATTC 120

QY 122 AGATGCTCCTTGGCTCTCCCTGTACGTCTACGCTTACGGATTC 121

Db 121 AGATGCTCCTTGGCTCTCCCTGTACGTCTACGGATTC 120

QY 182 CCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCT 181

Db 181 CCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCT 180

QY 241 CACACCTGGGGTGTGCGACATCGCCTACGCCATCGCTGCAACACGGTGCACGCCCT 240

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QY 541 TACCTTACCCCTCTGTAGGCCAGAAATTACACTTTTGTTGAAATCTGGCT 600

Db 541 TACCTTACCCCTCTGTAGGCCAGAAATTACACTTTTGTTGAAATCTGGCT 599

QY 601 GTTCTCAAACCTGGCTGCGAGATAACCAATCACATTGTGAAATCTGGCT 659

Db 601 GTTCTCAAACCTGGCTGCGAGATAACCAATCACATTGTGAAATCTGGCT 659

QY 661 ATTCTGGGCTGGGGACCTGTCCACAAATTGATGTCATATGTGATCCTCTGT 720

Db 660 ATTCTGGGCTGGGGACCTGTCCACAAATTGATGTCATATGTGATCCTCTGT 719

QY 721 GCTATCCTCAGATCCATCAAGGAAAGTCAGAGGAAGGCCTTCGACACTGTGTTCTCC 780

Db 720 GCTATCCTCAGATCCAAATCAAGGAAAGTCAGAGGAAGGCCTTCGACACTGTGTTCTCC 779

QY 781 CACCTCTGGTGTGACTCTTATGGCACAGCCATTATCATGTATGTGACATCTCTGT 840

Db 780 CACCTCTGGTGTGACTCTTATGGCACAGCCATTATCATGTATGTGACATCTCTGT 839

QY 841 TATGGAAACCCAAAGGAGCAGAAAGAATATCTCTGCTGTTCACAGCCTTTAACCC 900

Db 840 TATGGGAAACCCAAAGGAGCAGAAATATCTCTGCTGTTCACAGCCTTTAACCC 899

QY 901 ATGCTCAATCCCCATTCTGTAGTCTTAGGAACCTCAGAAAGTGAAGAATACTTTGAAGAGA 960

Db 900 ATGCTCAATCCCCATTCTGTAGTCTTAGGAACCTCAGAAAGTGAAGAATACTTTGAAGAGA 959

QY 961 GTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGGCATATGTGACTGACA 1013

Db 960 GTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGGCATATGTGACTGACA 1012

RESULT 5

US-09-898-586-3

; Sequence 3, Application US/09898586

; Publication No. US2003007794A1

; GENERAL INFORMATION:

; APPLICANT: Gerlach, Valerie L

; APPLICANT: MacDougal, John R

; APPLICANT: Smithson, Glenna

TITLE OF INVENTION: No. US2003007794A1el Polypeptides and Nucleic Acids Encoding FILE REFERENCE: 15966-638CIP

CURRENT APPLICATION NUMBER: US/09/898, 586

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/177, 839

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 60/176, 134

PRIOR FILING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: 60/175, 989

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: 60/218, 324

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/220, 253

PRIOR FILING DATE: 2000-07-24

PRIOR APPLICATION NUMBER: 60/178, 191

PRIOR FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/178, 227

PRIOR FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/220, 590

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: 09/761, 288

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 104

SOFTWARE: Patentin Ver. 2.1



; PRIORITY FILING DATE: 2000-01-26  
 ; PRIORITY APPLICATION NUMBER: 60/220,590  
 ; PRIORITY FILING DATE: 2000-07-25  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1040  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-761-288-3

Query Match 97.0%; Score 983.6; DB 10; Length 1040;  
 Best Local Similarity 99.4%; Pred. No. 9.2e-311; Mismatches 4; Indels 2; Gaps 2;  
 Matches 1008; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 TAAACACTCTCTAAACCTGAGATACCCACATCAATGAGAACATGGCTTGGGGAGC 659  
 Db 28 TAAACACTCTCTCTAAACCTGAGATACCCACATCAATGAGAACATGGCTTGGGGAGC 686  
 QY 61 GACAATATAACATCCATCACAGAGACTCTCTACTGGATTCCCGTTGGCCAAAGGATT 120  
 Db 88 GACAATATAACATCCATCACAGAGACTCTCTACTGGATTCCCGTTGGCCAAAGGATT 746  
 QY 121 CAGATGCTCTCTTGGCTCTCCCTGGTTCTACGTCTTCACCCCTGTTGGGGAAACGGG 207  
 Db 148 CAGATGCTCTCTTGGCTCTCCCTGGTTCTACGTCTTCACCCCTGTTGGGGAAACGGG 806  
 QY 181 ACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGGCCCTTGTGACTTC 239  
 Db 208 ACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGGCCCTTGTGACTTC 267  
 QY 240 TCACACCTGGGGTGTGACATGGGAAAGGATTATGGCATTTGACTGACA 899  
 Db 268 TCACACCTGGGGTGTGACATGGGAAAGGATTATGGCATTTGACTGACA 926  
 QY 300 AACCTCTGCATCCAGCCAGGCCATCTCCCTTGCGGCGCATGTCAGACCTTCTG 359  
 Db 328 AACCTCTGCATCCAGCCAGGCCATCTCCCTTGCGGCGCATGTCAGACCTTCTG 986  
 QY 360 TTTCACTTGTGTCAAGAGAATCTCTCTCTGGTGTCTATGATCTGTAC 419  
 Db 388 TTTCACTTGTGTCAAGAGAATCTCTCTCTGGTGTCTATGATCTGTAC 387  
 QY 420 GTGGCCATCTGCCACCCCTCGATATTGGCCATCATGACCTGGAGAGCTGTGATCACC 479  
 Db 448 GTGGCCATCTGCCACCCCTCGATATTGGCCATCATGACCTGGAGAGCTGTGATCACC 507  
 QY 480 CTCGGGTGACTCTCTGGACACTGGAGCTGGAGCTCCCTTATCCTGATTCATCTGTGTACTT 539  
 Db 508 CTCGGGTGACTCTCTGGACACTGGAGCTGGAGCTCCCTTATCCTGATTCATCTGTGTACTT 567  
 QY 540 CTACCTTACCCCTCTGTAGGCCAGAAATTATCACTTTTGTGAATCTGGC 599  
 Db 568 CTACCTTACCCCTCTGTAGGCCAGAAATTATCACTTTTGTGAATCTGGC 626  
 QY 600 TGTCTCAACTTGCCATGCGAGATAACCCACATCAAGGAAGGAAAGCTCTGGGGAGC 659  
 Db 627 TGTCTCAACTTGCCATGCGAGATAACCCACATCAAGGAAGGAAAGCTCTGGGGAGC 686  
 QY 720 TGCTATCCCTCAGATCCATCAAGGAAGGAAAGCTCATGAGAACATGGCTTGGCCGGAGC 719  
 Db 660 AATTCTGGGTGGGACCCCTGTCACAACTTGAGTTCATGAGAACATGGCTTGGCCGGAGC 746  
 QY 780 CCACCTCTGTGATGGACTCTTATGGCACAGCCATTATCATGAGAACATGGCTTGGCCGGAGC 839  
 Db 807 CCACCTCTGTGATGGACTCTGTTATGGCACAGCCATTATCATGAGAACATGGCTTGGCCGGAGC 866  
 QY 840 ATATGGAAACCCAAAGGAGAGAAATATCCTGGTTTCACAGCCCTTAACT 899

RESULT 7  
 US-09-761-288-3  
 ; Sequence 3, Application US/09761288  
 ; Patient No. US20020065405A1

GENERAL INFORMATION:  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Prayaga, Sudhirdas  
 APPLICANT: Taupier, Raymond J  
 APPLICANT: Mishra, Vishnu  
 APPLICANT: Tchernev, Velizar  
 APPLICANT: Spytek, Kimberly  
 APPLICANT: Li, Li  
 TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding Same  
 FILE REFERENCE: 15966-638  
 CURRENT APPLICATION NUMBER: US/09/761,288  
 CURRENT FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: 60/175,839  
 PRIOR FILING DATE: 2000-01-13  
 PRIOR APPLICATION NUMBER: 60/176,134  
 PRIOR FILING DATE: 2000-01-14  
 PRIOR APPLICATION NUMBER: 60/175,989  
 PRIOR FILING DATE: 2000-01-13  
 PRIOR APPLICATION NUMBER: 60/218,324  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: 60/220,253  
 PRIOR FILING DATE: 2000-07-24  
 PRIOR APPLICATION NUMBER: 60/178,191  
 PRIOR FILING DATE: 2000-01-26  
 PRIOR APPLICATION NUMBER: 60/178,227

Db 867 ATATGGGAAACCCCAAGGAGCAGAAGAAATATCTCCTGCTTACAGCCCTCTTAATCC 926  
 QY 900 CAGTCCTAATCCCTTATCTGTAGCTTAGGACTCAGAAGATACTTGAGAG 959  
 ; Sequence 34, Application US/09761288  
 ; Patent No. US20020065405A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Prayaga, Sudhirdas  
 ; APPLICANT: Taupier, Raymond J  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Li, Li  
 ; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 15966-638  
 ; CURRENT APPLICATION NUMBER: US/09/761,288  
 ; CURRENT FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: 60/177,839  
 ; PRIOR FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: 60/176,134  
 ; PRIOR FILING DATE: 2000-01-14  
 ; PRIOR APPLICATION NUMBER: 60/175,989  
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 ; PRIOR APPLICATION NUMBER: 60/218,324  
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 ; PRIOR APPLICATION NUMBER: 60/178,191  
 ; PRIOR FILING DATE: 2000-01-26  
 ; PRIOR APPLICATION NUMBER: 60/178,227  
 ; PRIOR FILING DATE: 2000-01-26  
 ; PRIOR APPLICATION NUMBER: 60/220,590  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 34  
 ; LENGTH: 1040  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-761-288-34

Query Match 97.0%; score 983.6; DB 10; length 1040;  
 Best Local Similarity 99.4%; Pred. No. 9.2e-311; Gaps 2;  
 Matches 1008; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 TAAACACTTCTCTAAACCATGAGCTTAACTGATTCCCTCTGTCAAGGGATATGGG 60  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

RESULT 8  
 US-09-761-288-34

Db 927 CATGCTCAATCCCTTATCTGTAGCTTAGGACTCAGAAGATACTTGAGAG 986  
 QY 960 ATGTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGCACTGTGACTGACA 1013  
 ; Sequence 34, Application US/09761288  
 ; Patent No. US20020065405A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Prayaga, Sudhirdas  
 ; APPLICANT: Taupier, Raymond J  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Li, Li  
 ; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 15966-638  
 ; CURRENT APPLICATION NUMBER: US/09/761,288  
 ; CURRENT FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: 60/177,839  
 ; PRIOR FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: 60/176,134  
 ; PRIOR FILING DATE: 2000-01-14  
 ; PRIOR APPLICATION NUMBER: 60/175,989  
 ; PRIOR FILING DATE: 2000-01-13  
 ; PRIOR APPLICATION NUMBER: 60/218,324  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/220,253  
 ; PRIOR FILING DATE: 2000-07-24  
 ; PRIOR APPLICATION NUMBER: 60/178,191  
 ; PRIOR FILING DATE: 2000-01-26  
 ; PRIOR APPLICATION NUMBER: 60/178,227  
 ; PRIOR FILING DATE: 2000-01-26  
 ; PRIOR APPLICATION NUMBER: 60/220,590  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 34  
 ; LENGTH: 1040  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-761-288-34

Query Match 97.0%; score 983.6; DB 10; length 1040;  
 Best Local Similarity 99.4%; Pred. No. 9.2e-311; Gaps 2;  
 Matches 1008; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Db 987 ATGTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGCACTGTGACTGACA 1040  
 QY 121 CAGATGCTCTCTTGGGCTCTCCCTGTCTACGTCTCACCTGCTGGGAACGGG 180  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

RESULT 9  
 US-09-864-761-13963/C

Db 328 AACCTCTGCATCCAGCAAGCCCATCTCCCTGGGGCGCATGTCAGACCTTCTG 359  
 QY 360 TTTCACTTTGCTCACAGAATGTCCTCTGGGTGATGCTCTATGATCTGAC 419  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 388 TTTTCACTTTGCTCACAGAATGTCCTCTGGGTGATGCTCTATGATCTGAC 447  
 QY 420 GTGGCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGCATCAC 479  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 448 GTGGGCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGCATCAC 507  
 QY 480 CTCGGGTGACTTCTGGACACTGGGACTCTGGAGCTCCCTTATCCTGTGATCATCTGTGTTACCT 539  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 508 CTCGGGTGACTTCTGGACACTGGGACTCTGGAGCTCCCTTATCCTGTGATCATCTGTGTTACCT 567  
 QY 540 CTACCTTACCCCTCTGTAGGCCAGAAATTATCACTTTTTGTAATCTGAC 599  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 568 CTACCTTACCCCTCTGTAGGCCAGAAATTATCACTTTTTGTAATCTGAC 626  
 QY 600 TGTCTCAAACTTGCCTGTCAGATACCCACATCAATGAGAACATGGTCTGGCCGGAGC 659  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 627 TGTCTCAAACTTGCCTGTCAGATACCCACATCAATGAGAACATGGTCTGGCCGGAGC 686  
 QY 660 AATTTCTGGGCTGGGACCCCTGTCACAAATTGTTGATATATGTCATCCTCTG 719  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 687 ATTTCTGGCTGGGACCCCTGTCACAAATTGTTGATATATGTCATCCTCTG 746  
 QY 720 TGCTATCCTCAGATCCAACTCAAGGAAGTTCAGAGGAAGCCCTCTGCACCTGCTTC 779  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
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 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 747 TGCTATCCTCAGATCCAACTCAAGGAAGTTCAGAGGAAGCCCTCTGCACCTGCTTC 806  
 QY 780 CCACCTCTGTGTCAGTGGACTCTTTATGGCACAGCATTATCATGATGTTGGACCCAG 839  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
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 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 807 CCACCTCTGTGTCAGTGGACTCTGGCACAGCATTATCATGATGTTGGACCCAG 866  
 QY 840 ATATGGAAACCCCAAGGAGCAGAAGAAATATCCTCTGCTGTTCACAGCCCTTTAACCC 899  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 867 ATATGGAAACCCCAAGGAGCAGAAGAAATATCCTCTGCTGTTCACAGCCCTTTAACCC 926  
 QY 900 CAGTCCTAATCCCTTATCTGTAGCTTAGGACTCAGAAGATACTTGAGAG 959  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

Db 987 ATGTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGGCATTGTAAGTGAAC 1040  
 QY 987 ATGTGCTGGAGTAGAAAGGGCTTATGAAAGGATTATGGCATTGTAAGTGAAC 1040  
 ; Sequence 13963, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotrax sequence Listing Engine vers. 1.1
; SEQ ID NO: 13963
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004889.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; US-09-864-761-13963

Query Match 53.7%; Score 545; DB 10; Length 1957;
Best Local Similarity 74.6%; Pred. No. 3.1e-17;
Matches 711; Conservative 0; Mismatches 240; Indels 2; Gaps 2;
QY 36 TTTCTCTGTCTAGGGATATGGGACAATAACATCCATCACAGATCCTCTACT 95
Db 1073 TTTCTTTTTCACAGGGAAATCGACAATGTCACAGAGTCCCTCTACT 1014
QY 96 GGGATTCCCTGGCCAAAGGATTCAGATGCTCTTGGCTCTCCCTGTTCTA 155
Db 1013 GGGATTCTCTGGGCCAAAGGATTCAGATGCTCTTGGCTCTCCCTGTTCTA 954
QY 156 CGTCTTCACCCCTGGGAAACGGGACCATACTGGGCTCATCTCACTGGACTCCAGCT 215
Db 953 TATCTCACCCCTGGGAAACGGGCCATCCTGGGCTCATCTCACTGGACTCCAGCT 894
Db 893 CCACACCCCCATGTACTTCTCCCTCACACCTGGCTGACATCGCCTACACCCG 834
QY 216 GCAAGCCCCC-TGTACTTCTCTCTCACACCTGGGCTGACATCGCCTACACCCG 274
Db 833 CAACACGGTCCCCAGATGCTGGGAACTCTGCTCATCCAGCCAAAGCCCATCTCCCTG 774
QY 335 GGGCCGATGATGCAAGACCTTCTGTTCACTTGTGTCACAGAAATGTCCTCTCT 394
Db 773 TGGTTGCAATGACGCAGACCTTCTGTTGAGTTGGACACAGCGAATGTCCTGCT 714
QY 395 GGTGGTGTATGTCCTATGATCTGTACGGGCCATCTGCCACCCCTCCGATACTCCGTCAT 654
Db 713 GGTGCTGATGTCCTACGATCGTGGCCATCTGCCACCCCTCCGATACTCCGTCAT 654
QY 455 CATGACCTGGAGAGTCTGCACTACCCCTCCGGGTGACTTCCTGGGACACTGGAGTCTTT 514
Db 653 CATGACCTGGAGAGTCTGCACTACCCCTCCGGGTGACTTCCTGGAGTCTTT 594
QY 515 ATCCTGATTCACTTGTGTTACTTCTACCTTACCCCTCTGAGGGCCAGAAATT 574
Db 593 GGCRCGGCCCATGTTCTCATCCTAAGACTGCCCCCTCTGGGCTCATGAAATCAA 534
QY 575 TCACTTTTGTGAATCTGGCTGTTCTCAACCTGCTGTGAGGAAATT 634
Db 533 CCAC-TCTCTCTGTAATCCTGTCAGGCTGGGCTGTGCTGACACCTGGCTCA 475
QY 635 ATGAGACATGGCTGGCCGGACATTCTGGCTGGGACCTTGTCAGATCCACATCA 694
Db 414 TTGTCCTACTCCACATCCCTGGGGCCATCTCTGAGGATCCAGTCTGGGGCCGCA 355
QY 695 TAGTTCTATATGTCATCCCTGTCATCCCTGTCATCTCTCAGATCCAATCAAGGAAGTCAGA 754
Db 354 GAAAGGCTTCTCACCTGCTCTCCACCTCTGCTGCTGCTGCTGCTGCTGCTG 295
QY 815 CCATTATCATGTTGGACCCAGATGGGAAACCCAAAGGAGCAGAAATATCTC 874
Db 294 CCATCATGTCATGTCATGGCCCAACTCCGGCATCTGAGGAGCAGCAAGGTCTT 235
QY 875 TGCTGTTACAGTTTCAACCCAAACCTTAACCCCTGATTTACAGCCTGAGGAAG 175
Db 234 TTCTATTTACAGTTTCAACCCAAACCTTAACCCCTGATTTACAGCCTGAGGAAG 175
QY 935 CAGAAGTGAAGAATACTTGAGAGAGTCTGGGAGTAGAAAGGCTTATGA 987
Db 174 GAGGGTCAAAGGGTGCCTGAGGAGCACTGGCAAGGAAGTCATTCTAA 122
; RESULT 10
; Sequence 92, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331

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; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO: 92  
; LENGTH: 2282  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: CDS  
; NAME/KEY: (1257)..(2189)  
; LOCATION: US-10-098-841-92

RESULT 11  
US-09-747-835A-62  
; Sequence 62, Application US/09747835A  
; Patent No. US20020146692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyian  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-  
; TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-37CIP  
; CURRENT APPLICATION NUMBER: US/09/747, 835A  
; PRIORITY APPLICATION NUMBER: US 09/729, 739  
; PRIORITY FILING DATE: 2000-12-04  
; PRIORITY APPLICATION NUMBER: US 09/653, 450  
; PRIORITY FILING DATE: 2000-03-08  
; PRIORITY APPLICATION NUMBER: US 09/620, 312  
; PRIORITY FILING DATE: 2000-07-19  
; PRIORITY APPLICATION NUMBER: US 09/598, 042  
; PRIORITY FILING DATE: 2000-06-20  
; PRIORITY APPLICATION NUMBER: US 09/552, 317  
; PRIORITY FILING DATE: 2000-04-25  
; PRIORITY APPLICATION NUMBER: US 09/488, 725  
; PRIORITY FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 62  
; LENGTH: 2282  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: CDS  
; NAME/KEY: (1257)..(2189)  
; LOCATION: US-09-747-835A-62

Query Match 53.1%; Score 538.2; DB 9; Length 2282;  
Best Local Similarity 73.6%; Pred. No. 5.6e-165; Mismatches 253; Indels 2; Gaps 2;

Qy 31 CTTGATTTCCTCTGTCATAGGGATATGGGGACAATAACATCCATCACAGAGTTCTC 90  
Db 1233 CTTGTTGTTTTAGTAGTGAAATGGTAAACATGGTCACAGAGTTCTC 1292  
Qy 91 CTACTGGATTCCGGTGGCCAGGGATCAGATGGCTCTTGGGCTTCTCCTG 150  
Db 1293 CTACTGGATTTCCTGGGCCAAGGATTCAGATGGCTCTTGGGCTTCTCCTG 1352  
Qy 151 TTCTAGTCTCACCCCTGCTGGGACCGGACATACTGGGCTCATCTCACTGGACTCC 210  
Db 1353 TTCTATGTCCTCACCCCTGCTGGGACCGGACATACTGGGCTCATCTCACTGGACTCC 1412  
Qy 211 AGACTGCACGGGG-TGTACTTCTCTCACACCTGGGGCTGTCACAGAGTTCTC 269  
Db 2132 GAATGTTAGGGTCAAGGGTGGAGGACACTGGTCAAGGAAGTCATTCTTAAG 2191  
Qy 990 AGGATA 996  
Db 2192 GGTGTA 2198

Query Match 53.1%; Score 538.2; DB 10; Length 2282;  
Best Local Similarity 73.6%; Pred. No. 5.6e-165; Mismatches 253; Indels 2; Gaps 2;

Qy 31 CTTGATTTCCTCTGTCATAGGGATATGGGGACAATAACATCCATCACAGAGTTCTC 90  
Db 1233 CTTGTTGTTTTAGTAGTGAAATGGTAAACATGGTCACAGAGTTCTC 1292  
Qy 91 CTACTGGATTCCGGTGGCCAGGGATCAGATGGCTCTTGGGCTTCTCCTG 150  
Db 1293 CTACTGGATTTCCTGGGCCAAGGATTCAGATGGCTCTTGGGCTTCTCCTG 1352  
Qy 151 TTCTACGTCTCACCCCTGCTGGGACCGGACATACTGGGCTCATCTCACTGGACTCC 210  
Db 1353 TTCTATGTCCTCACCCCTGCTGGGACCGGACATACTGGGCTCATCTCACTGGACTCC 1412  
Qy 211 AGACTGCACGGGG-TGTACTTCTCTCACACCTGGGGCTGTCACAGAGTTCTC 269  
Db 2132 GAATGTTAGGGTCAAGGGTGGAGGACACTGGTCAAGGAAGTCATTCTTAAG 2191  
Qy 870 TCTCCTGCTGTTACAGGCCTTTAATCCCATGCTCAATGCCCTTACTGTAGCTTAG 929  
Db 2012 CAGGCCATGTCATGTCATGCCCTAAGTCCCCTACAGGAGGACAGCAGAAGT 2071  
Qy 1413 AGACTCCACACCCCATGTCATCTCTCACACCTGGGGCTGTCACACATCGCTAT 1472  
Db 2072 CCTTTCTTACAGTCTTCAACCCGATGCTAACCCGATGCTAACCCCTGAG 2131

Db 1473 GCCTGCAACACAGTGCCCCAGATGCTGTAACCTCTGCATCCAGCCAAAGCCATCTCC 1532  
 Qy 330 TTTGGGGGGGGCATGATGAGACCTTCTGTTCCACTTGTGTCACAGAATGTC 389  
 Db 1533 TTTGCTGGCTGCATGACAGACCTTCTCTTGTGACATACTGAATGCTC 1592  
 Qy 390 CTCCGGGGATGTCATGATCTGTACGTGGCATCTGCCACCCCTCCGATATTG 449  
 Db 1593 CTGTTGGGGCATGTCATGACCTGGTACGGTACGCCATGCCACCTCCGATATTG 1652  
 Qy 450 GCCATCATGACCTGGAGAGTCTGCATCACCTCCGGTACTCTGGACACTGGAGTC 509  
 Db 1653 ATCATCATGACCTGGAAAGTCTGCATCACTCTGGCCATCACCTGGACATGTGCTC 1712  
 Qy 510 CTTTATCCATGATTCACTTGTGTTACTCTACCTTACCCCTGTAGGGCCAGAA 569  
 Db 1713 CTCTGGCTATGGTCCATGTCAGGCCCTCATCTTAAGACTGCCCTTGTGGCCTCGTGA 1772  
 Qy 570 ATTATCACTTTTGTGAATCTGGCTGTCAAACTGGCTGTCAGATACCC 629  
 Db 1773 ATCAACAC-TTCTTCTGTGAATCTCTGTCAGGCCCTGTGCTGATACCTG 1831  
 Qy 630 CATCAATGAGAACATGGTCTGGGGAGCAATTCTGGGTGTTGGGACACTCTGC 689  
 Db 1832 GCTCAACAGGGTGTCACTTGTGAGCCCTGCATGTTCATCTGGGGACACTCTGC 1891  
 Qy 690 AATTGTTGATTCATATATGTCATCCTCTGTGCTATCCTTCAGATCAAGGAACT 749  
 Db 1892 GGTGCTGGTCTCACTCACACATCTGGGGCATCTGTGAGATCCAGTCTGGGGAGG 1951  
 Qy 750 TCGAGGAAGCCTCTCACCTCTGTGTTAGACTCTTTATGG 809  
 Db 1952 CCGCAGAAGGCTCTCACCTCTGCTCCACCTCTGCTAGTGGACTCTTTGG 2011  
 Qy 810 CACGCCATTATCATGTTGACCCAGATATGGAAACCCAAAGGAGCAGAAATA 869  
 Db 2012 CAGGCCATGTCATGTCATGGCCCTAAGTCCGCCATCTGAGGAGCAGGAAGT 2071  
 Qy 870 TCTCCTGCTGTTCACAGCCTTTAATCCCATGCTCAATCCCTTATCTGTAGCTTAG 929  
 Db 2072 CCTTTCTATTTACAGTTCTCAACCCGATGCTAAACCCCTGATTACAACCTGAG 2131  
 Qy 930 GAACTCAGAGGTGAGAACTTGTGAGAGGTGCTGGAGTAGAAAGGGTTATGAA 989  
 Db 2132 GAATCTAGAGGTCAAGGGTGCCTGAGGAGACACTGTGCAAGAAGTCATCCCTAAGA 2191  
 Qy 990 AGGATTA 996  
 Db 2192 GGTGTGA 2198

RESULT 12

US-09-747-835A-35  
 Sequence 35, Application US/09747835A  
 Patent No. US20020146692A1

GENERAL INFORMATION:

- APPLICANT: Yamazaki, Victoria
- APPLICANT: Tang, Y. Tom
- APPLICANT: Liu, Chenghua
- APPLICANT: Zhou, Ping
- APPLICANT: Wang, Dunrui
- APPLICANT: Zhang, Jie
- APPLICANT: Ren, Feiyan
- APPLICANT: Asundi, Vinod
- APPLICANT: Drmanac, Radmila T
- APPLICANT: Drmanac, Radmila T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
 TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES  
 FILE REFERENCE: HYS-37CIP  
 CURRENT APPLICATION NUMBER: US/09/747,835A  
 CURRENT FILING DATE: 2002-03-08  
 PRIOR APPLICATION NUMBER: US 09/729,739  
 PRIOR FILING DATE: 2000-12-04

Qy 450 GCCATCATGACCTGGAGAGTCTGCATCACCTCGGGTACTCTGGACCACTGGAGTC 509  
 Db 881 ATCATCATGACCTGGAAAGTCTGCATCACTCTGGCCATCTGCCACCCATCTCC 940  
 Qy 510 CTTTATCCATGATTCATCTGTGTTACTCTACCTTACCTCTGTAGGGCCAGAA 569  
 Db 941 CTCTGGCTATGGTCCATGTCATCTGGACATGCCCTTGTGGGCTCGTGA 1000  
 Qy 570 ATTATCACTTTTGTGAATCTGGCTGTCAAACTTGCCGTGTCAGATACCC 629  
 Db 1001 ATCAACAC-TTCTCTGTGAATCCCTGTGCTGAGGCTGTCAGATACCC 880  
 Qy 630 CATCATGAGAACATGGTCTGGGGAGCAATTCTGGCTGGGGACCACTGTGTCAC 689  
 Db 1060 GCTCAACAGGGTGTCACTTGTGAGCCCTGCATGTTCATCCTGGGGACCACTGTGTCAC 1119  
 Qy 690 AATTGTTGATTCATATATGTCATCCTCTGCTACATCCTCAGATCAAGGAGT 749  
 Db 1120 GGTGCTGGTCTCTACACATCCTGGGGCATCTGAGGAGTCCAGTCTGGGGAGG 1179

PRIOR APPLICATION NUMBER: US 09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US 09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US 09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US 09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US 09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 35  
 LENGTH: 1788  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (833)..(1417)  
 US-09-747-835A-35

Query Match 52.9%; Score 536.6; DB 10; Length 1788;  
 Best Local Similarity 73.5%; Pred. No. 1.6e-164;  
 Matches 711; Conservative 0; Mismatches 254; Indels 2; Gaps 2;

Qy 31 CTTGATTCTCTGTCAAGGATATGGGGACAATAACATCCATCACAGAGTCC 90  
 Db 461 CTTGTTGTTTTAGTAGTGAATGGTGAATGGGAAATTCAGACATGGTCC 520  
 Qy 91 CTACTGGATTCCCGTGGCCAAAGGATTCAGATGCTCTCTTGGCTCTCTCC 150  
 Db 521 CTACGGATTCTCCTGGGCCAAAGGATTCAGATGCTCTCTTGGCTCTCC 580  
 Qy 151 TTCTACGTCTCACCCCTGCTGGGAACTGGGACCATACTGGGCACTCTC 210  
 Db 581 TTCTATGTCTCACCCCTGCTGGGAACTGGGACCATCTGGGCTCATCTC 640  
 Qy 211 AGACTSCACGGCCC-TGTACTCTCTCACACCTGGGTCGTCAGATGCC 269  
 Db 641 AGACTCCACACCCCATGTTCTCACACCTGGGGCTGTCACATGCC 700  
 Qy 270 GCCTGCAACACGGTGGCCCGATGCTGGACCTCTGCATCCAGCCACCCATCTCC 329  
 Db 701 GCCTGCAACACAGTGGCCAGATGCTGGTAACCTCTGCATCCAGCCACCCATCTCC 760  
 Qy 330 TTGCGGGCCGCATGATGCAAGACCTTGTGTTCCACTTTGTGTCACAGAATGTC 389  
 Db 761 TTGCTGGCTGCATGACATAGACATGACCTTCTCTTTGAGTTGACATACCTGAGTC 820  
 Qy 390 CCTCTGGGGCTGATGTCATCTGTCACGGCCATCTGCCACCCCTCCGATATTG 449  
 Db 821 CTGTTGGTGTGATGTCCTACGATCGGTACGTGGCCATCTGCCACCCCTCCGATATTG 880  
 Qy 450 GCCATCATGACCTGGAGAGTCTGCATCACCTCGGGTACTCTGGACCACTGGAGTC 509  
 Db 881 ATCATCATGACCTGGAAAGTCTGCATCACTCTGGCCATCTGCCACCCATCTCC 940  
 Qy 510 CTTTATCCATGATTCATCTGTGTTACTCTACCTTACCTCTGTAGGGCCAGAA 569  
 Db 941 CTCTGGCTATGGTCCATGTCATCTGGACATGCCCTTGTGGGCTCGTGA 1000  
 Qy 570 ATTATCACTTTTGTGAATCTGGCTGTCAAACTTGCCGTGTCAGATACCC 629  
 Db 1001 ATCAACAC-TTCTCTGTGAATCCCTGTGCTGAGGCTGTCAGATACCC 880  
 Qy 630 CATCATGAGAACATGGTCTGGGGAGCAATTCTGGCTGGGGACCACTGTGTCAC 689  
 Db 1060 GCTCAACAGGGTGTCACTTGTGAGCCCTGCATGTTCATCCTGGGGACCACTGTGTCAC 1119  
 Qy 690 AATTGTTGATTCATATATGTCATCCTCTGCTACATCCTCAGATCAAGGAGT 749  
 Db 1120 GGTGCTGGTCTCTACACATCCTGGGGCATCTGAGGAGTCCAGTCTGGGGAGG 1179

QY 750 TCAGAGGAAGCCTCTGCACCTGCTCTCCACCTCTGGTGATTGGACTCTTTATGG 809  
 Db 1180 CGCGAGAAAGGCCTCTCCACCTGCTCTCCACCTCTGGACTCTTTGG 1239  
 QY 810 CACGCCATTATCATGTATGGACCCAGATATGGAAACCCCAAGGAGCAGAAATA 869  
 Db 1240 CAGGCCATCGTCATGTACATGCCCTAAGTCCGCATCTGGTGAACCTCTGCATCC 1299  
 QY 870 TCTCTGCTGTTACAGCCTTTAATCCATGTCATAACCCCTATCTGTAGCTTAG 929  
 Db 1300 CCTTTCTTACAGTCTTCACCCGATGCTAACCCCTGTGAG 1359  
 QY 930 GAACTCAGAAGTGAAGATACTTGAAGAGAGTGCTGGAGTAGAAGGGCTTATGAA 989  
 Db 1360 GAATGTAGAGGTCAAGGGTGCCTGAGGAGAGCACTGTGCAAGGAAGTCATTCTAAGA 1419  
 QY 990 AGGATTA 996  
 Db 1420 GGTGTGA 1426

RESULT 13  
 US-09-747-835A-34  
 ; Sequence 34, Application US/09747835A  
 ; Patent No. US20020146692A1

; GENERAL INFORMATION:  
 ; APPLICANT: Yamazaki, Victoria  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Drmanac, Radivoje T  
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
 ; TITLE OF INVENTION: LIKE POLYPEPTIDES AND POLYNUCLEOTIDES  
 ; FILE REFERENCE: HYS-37CIP

CURRENT APPLICATION NUMBER: US/09/747, 835A  
 CURRENT FILING DATE: 2002-03-08  
 PRIOR APPLICATION NUMBER: US 09/729, 739  
 PRIOR FILING DATE: 2000-12-04  
 PRIOR APPLICATION NUMBER: US 09/653, 450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US 09/620, 312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US 09/598, 042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US 09/552, 317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US 09/488, 725  
 PRIOR FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 34  
 LENGTH: 2735  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-747-835A-34

Query Match 52.9%; Score 536.6; DB 10; Length 2735;  
 Best Local Similarity 73.5%; Pred. No. 2.1e-164; Mismatches 254; Indels 2; Gaps 2;

QY 31 CTGATTCTCTGTCAAGGATATGGGGACAATAACATCCATCACAGAGTCCTC 90  
 Db 1311 CTTGTGTTTTAGTGTAGTGAATCAGACAATGGTTCCTC 1370  
 QY 91 CTACTGGGATTCCCGTGGCCAAAGGATCAGATGCTCTTGGCTCTCCCTG 150  
 Db 1371 CTACTGGGATTCTCTGGCCCAAGGATCAGATGCTCTTGGCTCTCC 1430  
 QY 151 TTCTACGTCTCACCCGCTGGGGACGGACATACTGGGCTCATCTCACTGACTCC 210

RESULT 14  
 US-09-864-761-30527/C  
 ; Sequence 30527, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Shannon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Aenoma-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864, 761

Db 1431 TTCTATGTCTCACCCCTGCTGGGAATGGACCATCTGGGCTCATCTCACTGGACTCC 1490  
 QY 211 AGACTGCACGCC-TGTAATTCTCTCACACCTGGGGTGTGACATCGGCCTAC 269  
 Db 1491 AGACTCCACACCCCATGTACTCTCCCTCACACCTGGGGTGTCAACATGCCTAT 1550  
 QY 270 GCCTGCAACACGGTCCCCGGATGCTGGTGAACCTCTGCATCCAGCCAGCCCACATCTCC 329  
 Db 1551 GCCTGCAACACAGTCCCCAGATGCTGGTGAACCTCTGCATCCAGCCAGCCCACATCTCC 1610

QY 330 TTGCGGGCCGATGTCAGACCTTCTGTTCACTTTGCTGTACAGAATGTC 389  
 Db 1611 TTTGCTGGTGCATGACATAGACCTTCTCTTTGAGTTGCACATACTGAATGCCC 1670  
 QY 390 CTCTGGGGTGTGATGTCCTATGAACTGTGACAGTGGCCATCTGCCACCCCTCCGATATG 449  
 Db 1671 CTGTTGGTGTGATGTCCTACGATCGGTACGGGGCATCTGCCACCCCTCCGATATTC 1730  
 QY 450 GCCATCATGACCTGGAGACTGTCATCACCCCTGGGACTCTGGACACTGGAGTC 509  
 Db 1731 ATCATCATGACCTGGAAAGTCTGCATCACCTGGGACATGGCTCC 1790  
 QY 510 CTTTATCCTGTATTCTGTGTTACTCTTACCTTCTGTAGGCCAGAAA 569  
 Db 1791 CTCCCTGGCTATGGTCCATGTGAGCCTCATCTAAAGCTGCGCTTTGGCCCTGTC 1850  
 QY 570 ATTTATCACTTTTGTGAAATCTGGCTGTTCTCAAACCTGCCGTGAGATACCA 629  
 Db 1851 ATCAACAC-TTCTCTGTGAAATCCTGTCCTCAGGCTGGCTGTGATACTG 1909  
 QY 630 CATCAATGAGAACATGGCTCTGGCGGAGCAATTCTGGCTGGGGACCCCTGTGAC 689  
 Db 1910 GCTCAACCAAGGTGTCATCTTGGCAGCCGTCATGTCATCTGGGGACCACTCTGCCT 1969  
 QY 690 AATGTAGTTGATATGTCATCTGTGCTATCCAGATCAAATAGGGAGT 749  
 Db 1970 GGTGCTGGTCTACTCACACATCTGGCCATCTGGGACTCTGGGAGGG 2029  
 QY 750 TCAGAGGAAGCCTCTGCACCTGCTTCCCACCTCTGGGACTCTTATGG 809  
 Db 2030 CGCGAGAAAGCCTCTCCACCTGCTCTGGCCATCTGGGACTCTGGG 2089  
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 Db 2090 CAGCCCATCGTCATGTACATGGCCCTAAGTCCGGCATCTGGGAGCAGAAAGT 2149  
 QY 870 TCTCTGCTGTTACAGCTTCAACCCGATGCTTAACCCCTATCTGTAGCTTAG 929  
 Db 2150 CCTTTCTTATTTACAGCTTCAACCCGATGCTTAACCCCTGTATACACCTGAG 2209  
 QY 930 GAACTCAGAAGTGAAGATACTTGAAGAGAGTGTGGAGTAGAAAGGGTTATGAA 989  
 Db 2210 GAATGTAGAGGTCAGGGTGCCTGAGGAGACCTGTGCAAGGAAGTCATTCTAAGA 2269  
 QY 990 AGGATTA 996  
 Db 2270 GGTGTGA 2276



PRIOR APPLICATION NUMBER: US 09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US 09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US 09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US 09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US 09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 41  
 LENGTH: 1782  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (485)..(1411)  
 US-09-747-835A-41

Query Match Similarity 50.4%; Score 511.4; DB 10; Length 1782;  
 Best Local Similarity 72.7%; Pred. No. 2.8e-156;  
 Matches 703; Conservative 0; Mismatches 256; Indels 8; Gaps 3;

Qy 31 CTTGATTCCCTCTGTCAAGGGATATGGGGACAATAACATCCATCACAGAGTTCTC 90  
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Qy 151 TTCTACGGCTCACCCCTGCTGGGAACGGGACCATACTGGGCTCATCTCACTGGACTCC 210  
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Qy 330 TTGCGGGGCCATGATGTCAGACCTTCTGTTTCCACTTTGCTGTACAGAATGTC 389  
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Qy 450 GCCATCATGACCTGGAGGTCTGCATCACCTGGGTGACTCTCTGGACCACTGGAGTC 509  
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Qy 690 AATTTGTTGATATGTCATCTCTGTGCTATCTCAGATCCAAATCAAGGGAAT 749  
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Search completed: May 2, 2003, 06:42:32  
 Job time : 1681 secs



OM of: US-09-898-586-24 to: Issued\_Patents\_NA:\*

out\_format : pfs

Date: Aug 21, 2002 8:19 PM

About: Results were produced by the GenCore software, version 4.5,

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Command line parameters:

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 -Q-/cgn2\_1/USPTO\_spool/US09898586/runat\_16082002\_205735\_20570/app\_query.fasta\_1.373  
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Search information block:

Query: US-09-898-586-24

Database: Issued\_Patents\_NA:\*

Database sequences: 3B3533

Database length: 122816752

Search time (sec): 45.940000

score\_list:

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seq\_documentation\_block:

; Sequence 1, Application US/08457948A

; Patent No. 5998164

; GENERAL INFORMATION:

; APPLICANT: LI, YI

; APPLICANT: CAO, LIANG

; APPLICANT: NI, JIAN

; APPLICANT: GENTZ, REINER

; APPLICANT: BULT, CAROL J.

; APPLICANT: SUTTON IIT, GRANGER G.

; APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

TITLE OF INVENTION: Coupled Receptor GPR2

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,948A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC R.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 116..1003

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alignment\_scores:

Quality: 1048.50

Length: 305

Ratio: 4.017

Gaps: 4

Percent Similarity: 85.574

Percent Identity: 69.180

alignment\_block:

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128 ATGGTCAAATCAGACATGGCACAGAGTCTCTACTGGGATTCT 177

17 ovalglyProArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPhe 34

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178 CCTGGGCCAAGGATTCAGATGCTCTTGGGCTCTCTCCCTGTTCT 227

34 YRVALPHETHRLEUGLYASNGLYTHRILEUGLYLEUERLEU 50

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228 ATGTCCTCACCCCTGCTGGGAATGGGACCATCCTGGGCTCATCTCAGT 277

51 ASPSERARGLEUHISALAProMetTyrPhePheLeuSerHisLeu 67

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278 GACTCCAGACTCCACACCCCCATGTACTCTCTCTCACACCTGGCGT 327

67 IVALASPILEALATYRALAlysAsnThrValProArgMetLeuVal 84

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84 EULEUHISPTOALALysProIleSerPheAlaValThrGluCysLeu 100

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378 TCCTGCATCCAGCCAAAGCCATCTCTTGTCTGGTGCATGAC 427

101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMe 117

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428 TTTCCTTPTTGAAGTPTGACACATACTGAAATGCCCTCTGGTGCAT 477

117 TSETRYASPLEUTYRVALALILECYSHISPROLEUARGTYRLEUAI 134

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478 GTCCTACATCGGTACGTGGCCATCTGCCACCCCTCTCCGATATTTCATCA 527

134 IEMETTHRTPARGVALCYSILETHRLVALRSETRPHTHRTHR 150

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528 TCATGACCTGGAAAGTCTGCACTCTGGCATCTACTTCCTGAGCATGT 577

151 GLYVALLEULeuSerLeuIleHisLeuValLeuLeuPheLeuProPh 167

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628 TTGTCGGCCTCGTGAATCAACCACTCTCTGIGAATCCTGTCGTGCC 677

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 seq\_documentation\_block:  
 Sequence 1, Application US/08467947A  
 Patent No. 6090575  
 GENERAL INFORMATION:  
 APPLICANT: LI, YI  
 APPLICANT: CAO, LIANG  
 APPLICANT: NI, JIAN  
 APPLICANT: GENTZ, REINER  
 APPLICANT: BULT, CAROL J.  
 APPLICANT: SUTTON III, GRANGER G.  
 APPLICANT: ROSEN, CRAIG A.  
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
 TITLE OF INVENTION: Coupled Receptor GPR1  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENT RELEASE #1.0, VERSION #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,947A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 4335  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04079  
 FILING DATE: 30-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1140002/ERK/KLM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1713 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 116..1003  
 US-08-467-947A-1

alignment\_scores:

Quality: 1048.50 Length: 305

Ratio: 4.017 Gaps: 4

Percent Similarity: 85.574 Percent Identity: 69.180

alignment\_block:

US-09-898-586-24 x US-08-467-947A-1 ..

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17 ovalglyProArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPhe 34

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178 CCTGGGCCAAGGATTCAGATGCTCTCTTGGGCTCTCTCCCTGTTCT 227

